

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 29, 2002, 16:03:34 ; Search time 23.62 Seconds

(without alignments)
348.101 Million cell updates/sec

Title: US-09-978-189-370

Perfect score: 1 MSLLPRRPPVSMRLAAL.....TKRFTKYNANMKRYEE 111

Sequence: BLOSUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /Geneseg/1101:*
2: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT:*
3: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT:*
4: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT:*
5: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT:*
6: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT:*
7: /SIDS8/gcgdata/geneseq/geneseq/AA1985.DAT:*
8: /SIDS8/gcgdata/geneseq/geneseq/AA1986.DAT:*
9: /SIDS8/gcgdata/geneseq/geneseq/AA1987.DAT:*
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11: /SIDS8/gcgdata/geneseq/geneseq/AA1989.DAT:*
12: /SIDS8/gcgdata/geneseq/geneseq/AA1990.DAT:*
13: /SIDS8/gcgdata/geneseq/geneseq/AA1991.DAT:*
14: /SIDS8/gcgdata/geneseq/geneseq/AA1992.DAT:*
15: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT:*
16: /SIDS8/gcgdata/geneseq/geneseq/AA1994.DAT:*
17: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT:*
18: /SIDS8/gcgdata/geneseq/geneseq/AA1996.DAT:*
19: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT:*
20: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT:*
21: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT:*
22: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT:*
23: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	587	100.0	111	AA41739	Human PRO273 prote
2	587	100.0	111	AA428290	Tim-1 protein. Ho
3	587	100.0	111	AA444295	Human PRO273 (UNC2
4	587	100.0	111	AA33423	Human PRO273 prote
5	587	100.0	111	AA88478	Human membrane or
6	582	99.1	111	AA29291	Human neokine-1.
7	527	89.8	99	AA31612	Human neokine-1.
8	522	88.9	99	AA29292	Human chemokine al
9	509	86.7	95	AA76089	Human CXC chemokine
10	509	86.7	95	AA505371	Human hux1 protein
11	509	86.7	95	AA56028	Skin cell protein,

19 hits
over 80%

12	506	86.2	99	AA31613	Murine neokine-1.
13	506	86.2	99	AA76085	Murine CXC chemokine
14	506	86.2	99	AA76115	Full-length murine
15	506	86.2	99	AA56024	Skin cell protein,
16	506	86.2	99	AA56024	Skin cell protein,
17	506	86.2	99	AA56024	Skin cell protein,
18	506	86.2	99	AA56024	Skin cell protein,
19	506	86.2	99	AA56024	Skin cell protein,
20	506	86.2	99	AA56024	Skin cell protein,
21	431	73.4	78	AA31614	Revised partial ro
22	428	72.9	77	AA76091	Partial rodent che
23	428	72.9	77	AA76091	Rat neokine-1. Ra
24	424	72.2	77	AA76090	hux1 fragment (re
25	424	72.2	77	AA76090	Skin cell protein,
26	424	72.2	77	AA76090	murks1 fragment (re
27	383	65.3	202	AA56029	Mouse murks1 protei
28	337	55.7	123	AA56434	Skin cell protein,
29	298	50.8	133	AA75979	Human colon cancer
30	298	50.8	133	AA75979	Partial alternativ
31	208	35.4	44	AA55918	Murine skin cell p
32	143	24.4	100	AA32558	Skin cell protein,
33	138	23.5	100	AA90928	Peptide #6595 enco
34	138	23.5	100	AA90928	Neutrophil chemota
35	138	23.5	100	AA90928	Macrophage derived
36	128	21.9	102	AA70793	Murine macrophage
37	128	21.9	107	AA70793	Gro-beta/MLP-2- α lp
38	128	21.9	107	AA70793	Human macrophage 1
39	128	21.9	107	AA70793	Human macrophage 1
40	128	21.9	107	AA70793	Human Gro beta cyt
41	128	21.9	107	AA70793	Growth related onc
42	128	21.9	131	AA25812	Human chemokine GR
43	117	20.0	107	AA70792	Human protein sequ
44	117	20.0	107	AA70792	Melanoma growth st
45	117	20.0	107	AA70792	Growth related onc

ALIGNMENTS

RESULT 1	AA41739	standard. Protein; 111 AA.
ID	AA41739	
AC	AA41739	
XX		
DT	07-DEC-1999	(first entry)
XX		
DE	Human PRO273 protein sequence.	
XX		
KW	Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;	
KW	probe; blood coagulation disorder; cancer; cellular adhesion disorder;	
KW	secreted protein; transmembrane protein.	
XX		
OS	Homo sapiens.	
XX		
PN	W09946281-A2.	
XX		
PD	16-SEP-1999.	
XX		
PF	08-MAR-1999;	99MO-US05028.
XX		
PR	10-MAR-1998;	98US-0077450.
PR	11-MAR-1998;	98US-0077632.
PR	11-MAR-1998;	98US-0077641.
PR	11-MAR-1998;	98US-0077649.
PR	12-MAR-1998;	98US-0077791.
PR	13-MAR-1998;	98US-0078004.
PR	17-MAR-1998;	98US-0078004.
PR	20-MAR-1998;	98US-0078886.
PR	20-MAR-1998;	98US-0078910.
PR	20-MAR-1998;	98US-0078935.
PR	20-MAR-1998;	98US-0078939.
PR	25-MAR-1998;	98US-0079294.

Murine neokine-1.
Murine CXC chemokine
Full-length murine
Skin cell protein,
Skin cell protein,
Skin cell protein,
Skin cell protein,
Skin cell protein,
Macaque neokine-1.
Revised partial ro
Partial rodent che
Rat neokine-1. Ra
hux1 fragment (re
Skin cell protein,
murks1 fragment (re
Mouse murks1 protei
Skin cell protein,
Human colon cancer
Partial alternativ
Murine skin cell p
Skin cell protein,
Peptide #6595 enco
Neutrophil chemota
Macrophage derived
Murine macrophage
Gro-beta/MLP-2- α lp
Human macrophage 1
Human macrophage 1
Human Gro beta cyt
Growth related onc
Human chemokine GR
Human protein sequ
Melanoma growth st
Growth related onc
Human chemokine GR

PR	26-MAR-1998	9805-0079656
PR	27-MAR-1998	9805-0079663
PR	27-MAR-1998	9805-0079664
PR	27-MAR-1998	9805-0079689
PR	27-MAR-1998	9805-0079728
PR	27-MAR-1998	9805-0079786
PR	30-MAR-1998	9805-0079920
PR	30-MAR-1998	9805-0079923
PR	31-MAR-1998	9805-0080105
PR	31-MAR-1998	9805-0080107
PR	31-MAR-1998	9805-0080194
PR	01-APR-1998	9805-0080327
PR	01-APR-1998	9805-0080328
PR	01-APR-1998	9805-0080334
PR	01-APR-1998	9805-0080334
PR	08-APR-1998	9805-00801049
PR	08-APR-1998	9805-0081071
PR	08-APR-1998	9805-0081071
PR	09-APR-1998	9805-0081193
PR	09-APR-1998	9805-0081203
PR	09-APR-1998	9805-0081229
PR	15-APR-1998	9805-0081336
PR	15-APR-1998	9805-0081352
PR	15-APR-1998	9805-0081355
PR	21-APR-1998	9805-0082568
PR	21-APR-1998	9805-0082569
PR	22-APR-1998	9805-0082700
PR	22-APR-1998	9805-0082704
PR	22-APR-1998	9805-0082804
PR	23-APR-1998	9805-0082767
PR	23-APR-1998	9805-0082796
PR	27-APR-1998	9805-0083332
PR	28-APR-1998	9805-0083336
PR	29-APR-1998	9805-0083392
PR	29-APR-1998	9805-0083495
PR	29-APR-1998	9805-0083530
PR	29-APR-1998	9805-0083545
PR	29-APR-1998	9805-0083558
PR	29-APR-1998	9805-0083559
PR	07-MAY-1998	9805-0084627
PR	07-MAY-1998	9805-0084637
PR	07-MAY-1998	9805-0084639
PR	07-MAY-1998	9805-0084643
PR	13-MAY-1998	9805-0085324
PR	13-MAY-1998	9805-0085338
PR	13-MAY-1998	9805-0085339
PR	15-MAY-1998	9805-0085573
PR	15-MAY-1998	9805-0085578
PR	15-MAY-1998	9805-0085580
PR	15-MAY-1998	9805-0085582
PR	15-MAY-1998	9805-0085659
PR	15-MAY-1998	9805-0085697
PR	15-MAY-1998	9805-0085704
PR	18-MAY-1998	9805-0086023
PR	22-MAY-1998	9805-0086392
PR	22-MAY-1998	9805-0086414
PR	22-MAY-1998	9805-0086430
PR	22-MAY-1998	9805-0086486
PR	28-MAY-1998	9805-0087096
PR	28-MAY-1998	9805-0087108

PR	28-MAY-1998:	98US-0087208.
PR	30-JUL-1998:	98US-0094651.
PR	11-SEP-1998:	98US-0100038.
PA	(GENTH) GENENTECH INC.	
PI	WOOD WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;	
XX		
DR	WPI: 1999-551358/46.	
DR	N-PDB; AA234205.	
XX		
PT	New secreted and transmembrane polypeptides and their polynucleotides,	
PT	useful for treating blood coagulation disorders, cancers and cellular	
PT	adhesion disorders -	
XX		
PS	Claim 12, Fig 149, 530pp; English.	
XX		
CC	The present invention describes secreted and transmembrane polypeptides	
CC	and their polynucleotides. The nucleotide sequences are useful as	
CC	sources of probes, primers, for chromosome mapping, and for generation	
CC	of antisense sequences. They can also be used to create transgenic	
CC	animals. The proteins can be used to treat a variety of diseases and	
CC	disorders, depending on their function. Diseases that may be treated	
CC	include blood coagulation disorders, cancers and cellular adhesion	
CC	disorders. They may also be used to raise antibodies. AA233891 to	
CC	AA234338, and AA41685 to AA41774 represent polynucleotide and	
CC	polypeptide sequence given in the exemplification of the present	
CC	invention.	
SQ	Sequence 111 AA:	
Query Match	100.0%; Score 587; DB 20; Length 111;	
Best Local Similarity	100.0%; Pred. No.2.3e-60;	
Matches 111; Conservative	0; Mismatches 0; Indels 0; Gaps	0.
YQ	1 MSLLPRAPVSRRLAALLLLTLATYARVDGSKCKSRKGPRTSYDVKKLEMKPKY 60	
Db	1 msllprappvsrmliaaaallllyarvdgskckcsrkglrysdvkklempky 60	
YQ	61 PHECEKWITTTKSVSRYRGQEHCLHPKLQSTKRFIKWYNANNEKRRVVEE 111	
Db	61 phceekwilttksvsryrgqehclhpklqstkrfikwynamekrrvyee 111	
RESULT 2		
ID	AA28290 standard; Protein; 111 AA.	
AC	AA28290;	
XX		
DT	28-SEP-1999 (first entry)	
DE	Tim-1 protein.	
KM	Chemokine; CXCR; Tim-1; inflammation; heart attack; stroke; infection; ss;	
KM	trauma; radiation; burns; frostbite; corrosive chemical; gene therapy.	
OS	Homo sapiens.	
PN	WO933990-A1.	
PD	08-JUL-1999.	
PF	14-DEC-1998; 98WO-US26546.	
PR	30-DEC-1997; 97US-0068955.	
PA	(CHIR) CHIRON CORP.	
PI	Chen TT, Kassam A, Pot D;	
OR	WPI: 1999-430244/36.	

DR N-PSDB; AAX89708.
 XX
 PT A new human CXG chemokine, Tim-1, useful for treating inflammation
 XX
 PS Claim 1; Page 43; 46pp; English.
 CC
 CC This is the amino acid sequence for the Tim-1 CXG chemokine. The Tim-1
 CC gene can be used to design therapeutic tools for treating inflammation
 CC due to stimuli such as heart attacks and stroke, infection, physical
 CC trauma, UV or ionizing radiation, burns, stroke, infection, physical
 CC chemicals. The Tim-1 gene and subgenomic polynucleotides can be used
 CC in gene therapy.
 CC
 XX
 SO Sequence 111 AA:
 Query Match 100.0%; Score 587; DB 20; Length 111;
 Best Local Similarity 100.0%; Pred. No. 2.3e-60;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSLLPRAPVSMRLAALLLLALYARVDGSKCCKSRGPKIRYSDVKLEMKPKY 60
 DB 1 msllprapvsmrllaaalllllalytarvdgskcksrkpkirysdvkklmkpkxy 60
 QY 61 PHEEKKWVITTTKSVSRGGEHCLHPKLOSTRKRTKYNMNEKRRVYEE 111
 DB 61 pheeekmwilttksvsryggehclhpklostrkrtkrynmnekrvye 111
 RESULT 3
 ID AAB44295 standard; Protein; 111 AA.
 AC AAB44295;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Human PRO273 (UNQ240) protein sequence SEQ ID NO:370.
 XX
 KW Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;
 KW expressed sequence tag; detection; cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200053756-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 18-FEB-2000; 2000WO-US04341.
 XX
 PR 08-MAR-1999; 99WO-US05028.
 PR 12-MAR-1999; 99US-0123957.
 PR 29-MAR-1999; 99US-0126773.
 PR 21-APR-1999; 99US-0130232.
 PR 28-APR-1999; 99US-0131445.
 PR 14-MAY-1999; 99US-0134287.
 PR 23-JUN-1999; 99US-0141037.
 PR 26-JUL-1999; 99US-0145698.
 PR 29-OCT-1999; 99US-0162506.
 PR 30-NOV-1999; 99WO-US28313.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30095.
 PR 30-DEC-1999; 99WO-US31243.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;

PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
 PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
 PI Shelton DL, Stewart RA, Tumas D, Williams PM, Wood WI;
 XX
 DR WPI: 2000-611443/58.
 DR N-PSDB; AAC78551.
 XX
 PT Novel PRO polypeptides and polynucleotides used in detection methods,
 PT to target bioactive molecules to specific cells, and to modulate
 PT cellular activities -
 PS Claim 12; Fig 149; 636pp; English.
 XX
 CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed
 CC sequence tag) sequences which encode secreted or transmembrane PRO
 CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic
 CC activity. The polynucleotides and polypeptides can be used for detecting
 CC the presence of PRO polypeptides in samples, for linking bioactive
 CC molecules to cells and for modulating biological activities of cells,
 CC using the polypeptides for specific targeting. The polypeptide targeting
 CC can be used to kill the target cells, e.g. for the treatment of cancers.
 CC The polypeptide pairs provide specific targeting of bioactive molecules
 CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
 CC the isolation of the PRO polynucleotide sequences.
 XX
 SQ Sequence 111 AA:
 Query Match 100.0%; Score 587; DB 21; Length 111;
 Best Local Similarity 100.0%; Pred. No. 2.3e-60;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSLLPRAPVSMRLAALLLLALYARVDGSKCCKSRGPKIRYSDVKLEMKPKY 60
 DB 1 msllprapvsmrllaaalllllalytarvdgskcksrkpkirysdvkklmkpkxy 60
 QY 61 PHEEKKWVITTTKSVSRGGEHCLHPKLOSTRKRTKYNMNEKRRVYEE 111
 DB 61 pheeekmwilttksvsryggehclhpklostrkrtkrynmnekrvye 111
 RESULT 4
 ID AAB33423 standard; Protein; 111 AA.
 AC AAB33423;
 XX
 DT 29-JAN-2001 (first entry)
 XX
 DE Human PRO273 protein UNQ240 SEQ ID NO:46.
 XX
 KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;
 KW dermatological; antiaarthritic; antirheumatic; immunosuppressive;
 KW haemostatic; antithyroid; antidiabetic; noctropic; neuroprotective;
 KW antianaemic; hepatotropic; vituicidic; antiproliferic; antiallergic;
 KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
 KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
 KW autoimmune thrombocytopenia; immune-mediated renal disease;
 KW demyelinating disease; hepatobiliary disease; Whipple's disease;
 KW inflammatory bowel disease; gluten-sensitive enteropathy;
 KW autoimmune disease; immune-mediated skin disease; allergic disease;
 KW immunological disease; transplantation associated disease;
 KW graft rejection; graft-versus-host-disease.
 OS Homo sapiens.
 XX
 PN WO200053758-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 02-MAR-2000; 2000WO-US05841.

XX 08-MAR-1999; 99WO-US05028.
 PR 10-MAR-1999; 99US-0123618.
 PR 12-MAR-1999; 99US-0123957.
 PR 23-MAR-1999; 99US-0125775.
 PR 12-APR-1999; 99US-0128849.
 PR 20-APR-1999; 99WO-US08615.
 PR 28-APR-1999; 99US-0133445.
 PR 04-MAY-1999; 99US-0133771.
 PR 14-MAY-1999; 99US-0134287.
 PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 28-JUL-1999; 99US-0146222.
 PR 01-SEP-1999; 99WO-US20111.
 PR 08-SEP-1999; 99WO-US20594.
 PR 13-SEP-1999; 99WO-US20944.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 05-OCT-1999; 99WO-US23089.
 PR 29-OCT-1999; 99US-0162506.
 PR 29-NOV-1999; 99WO-US28214.
 PR 30-NOV-1999; 99WO-US28313.
 PR 30-NOV-1999; 99WO-US28409.
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28531.
 PR 02-DEC-1999; 99WO-US28564.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30999.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
 PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
 PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
 XX
 DR N-PSDB; AAC58588.
 XX
 WIPI: 2000-572271/53.
 PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -
 XX
 PS Claim 33; Fig 20; 309pp; English.
 XX
 CC The present invention describes sixty four human PRO proteins which can
 CC be used in the treatment of immune related diseases. The human PRO
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
 CC treating and diagnosing immune related disorders. The disorders are
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
 CC immune-mediated renal disease, demyelinating diseases of the central
 CC and peripheral nervous systems, hepatobiliary diseases, inflammatory
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,
 CC autoimmune or immune-mediated skin diseases, allergic diseases,
 CC immunological diseases of the lung, and transplantation associated
 CC diseases including graft rejection and graft-versus-host-disease.
 CC AAC5397 to AAC58578 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and

CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.
 XX
 SQ Sequence 111 AA;
 Query Match 100.0%; Score 587; DB 21; Length 111;
 Best Local Similarity 100.0%; Pred. No. 2,3e-60;
 Matches 111: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSLLPRRAPVSMRLAALLLLALYARVDSKCKSCSKGKIRYSDVKIKLEMPKY 60
 DB 1 msllprapvsmrllaaallllalylarvdsckscskgkirkysdvkiklemkpy 60
 QY 61 PHCEEKWIIITTKSVSRRYGEOHCILPKLOSTKRFIRKMYNMMNKKRYVEE 111
 DB 61 phceekwiltksvsrtrygehcilpklqstkrfirkmywnmmkrryvee 111
 Db
 RESULT 5
 ID AAB88478 standard; Protein: 111 AA.
 XX
 AC AAB88478;
 XX
 DT 23-MAY-2001 (first entry)
 XX
 DE Human membrane or secretory protein clone PSEC0212.
 XX
 KM Human; secretory protein; membrane protein; vaccine; gene therapy;
 KM rheumatoid arthritis; diabetes.
 OS Homo sapiens.
 PM EPI067182-A2.
 PD 10-JAN-2001.
 XX
 PF 07-JUL-2000; 2000EP-0114090.
 XX
 PR 08-JUL-1999; 99JP-0194179.
 PR 11-JAN-2000; 2000JP-0118775.
 PR 02-MAY-2000; 2000JP-0183766.
 XX
 PA (HELI-) HELIX RES INST.
 PI Ota T, Isogai T, Nishikawa T, Kawai Y, Sugiyama T, Hayashi K;
 DR
 DR WIPI: 2001-093989/71.
 DR N-PSDB; AAF93905.
 XX
 PT Nucleic acids encoding secretory proteins/membrane proteins, useful in
 PT gene therapy or as candidate target molecules in drug development -
 XX
 PS Claim 1; SEQ ID 324; 609pp + CD ROM; English.
 XX
 CC This invention relates to nucleic acid sequences AAF93744 - AAF93916
 CC which encode human secretory or membrane proteins represented by
 CC AAB88317 - AAB88419. Included in the invention are primers
 CC AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the
 CC cDNA sequences of the invention. The invention also includes methods for
 CC the production of antibodies directed against the proteins, and cDNA
 CC sequences, which can be used in vaccines. The polynucleotide sequences
 CC can be used in gene therapy. The polynucleotide sequences and the
 CC proteins they encode may be used in the prevention, treatment and
 CC diagnosis of diseases associated with inappropriate secretory
 CC protein/membrane protein expression. The nucleic acids and complementary
 CC sequences may also be used as DNA probes in diagnostic assays
 CC (e.g. polymerase chain reactions (PCR)) to detect and quantitate the
 CC presence of similar nucleic acid sequences in samples. They may also be
 CC used to study the expression and function of secretory proteins/membrane
 CC polypeptides and their role in metabolism. The polypeptides may be used
 CC as antigens in the production of antibodies against them and in assays to

CC used to assemble two non-overlapping contigs. To establish that
 CC these two contigs derived from the same transcript, two
 CC primers were designed to amplify the region between these contigs.
 CC These primers were h112/227f (AAZ08966) and h112/526r (AAZ08967).
 CC To obtain a full open reading frame (ORF), the 5' end of the single
 CC contig was generated via the RACE (rapid amplification of cDNA ends)
 CC procedure, using primer h123racc1 (AAZ08968). The neokines are a novel
 CC family of chemottractant cytokines (chemokines) and are ligands for
 CC previously identified putative G protein-coupled receptor termed RDC1
 CC (also called the neokine receptor). The neokines are members of the
 CC non-ELR-CXC subfamily of chemokines characterised by the absence of an
 CC ELR motif and the presence of a CXC signature motif. The CXC motif
 CC encompasses 4 highly conserved cysteine residues, with the first two
 CC cysteines separated by one non-conserved amino acid residue; however,
 CC the neokines show some atypical features which distinguish them from
 CC previously characterised CXC chemokines e.g., the presence of
 CC approximately 5 residues between the third and fourth conserved
 CC cysteines. The neokines have a variety of functions, including
 CC modulation of signal transduction, inhibition of angiogenesis,
 CC regulation of inflammation and inhibition of chemotraction.
 CC Neokines may therefore be useful in the treatment of various
 CC proliferative disorders or diseases: several types of cancer,
 CC inflammation, psoriasis, and immune rejection following skin graft
 CC and kidney transplantation. Neokines, their associated polynucleotides,
 CC homologues and antibodies can be used in screening for drugs or
 CC compounds which modulate their activity and therefore may be important
 CC for the development of new therapeutics.

Sequence 99 AA;

Query Match 89.8%; Score 527; DB 20; Length 99;
 Best Local Similarity 100.0%; Pred. No. 1.8e-53;
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 MRLIAAALLLLALYTAARDVDSKCKSRKGPRTIRYSDVKLEMKPRYPHCEKVIIT 72
 Db 1 mrliaaalllllalytarvdgskcksrkqklyrsvdkklemkpkypheekmvlitc 60

QY 73 KVSRYRGQEHCLHPKLOSTKRTIKWYNAMNEKRRVYEE 111
 Db 61 kvsryrgqehclhpklgstkrfkikwynamnekrvryee 99

RESULT 8

AAW29292 standard; Protein; 99 AA.

AAW29292;

14-APR-1998 (first entry)

Human chemokine alpha-2.

Human chemokine alpha-2; Ckalpha-2; treatment; prevention; tumour;
 Leukemia; T-cell mediated autoimmune disease; parasitic infection;
 psoriasis; asthma; allergy; haematopoiesis regulation;
 growth factor stimulation; angiogenesis inhibition;
 wound healing promotion; antagonist; rheumatoid arthritis;
 autoimmune disease; inflammatory disease; infective disease;
 allergic reaction; prostaglandin-independent fever;
 bone marrow failure.

Homo sapiens.

Location/Qualifiers

Peptide

Peptide

Peptide

MO9735010-A1.

PD 25-SEP-1997.
 XX
 PF 19-MAR-1997; 97WO-US04329.
 XX
 PR 19-MAR-1996; 96US-0013653.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Gentz RL, LI H, NI J, SU JY;
 XX
 DR WPI: 1997-480216/44.
 DR N-PSDB; AAT86316.
 XX
 PT Novel human chemokine alpha 2 and DNA encoding it - useful for
 PT treatment of leukaemia, tumours, autoimmune disease, wound healing,
 PT psoriasis, chronic infections and fibrotic disorders
 XX
 PS Claim 14; Pages 66-67; 82pp; English.
 XX
 CC The present sequence is human chemokine alpha-2 (Ckalpha-2),
 CC which can be used to treat and/or prevent tumours, leukaemia,
 CC T-cell mediated autoimmune diseases, parasitic infections,
 CC psoriasis, asthma and allergy, regulate haematopoiesis, stimulate
 CC growth factor activity, inhibit angiogenesis and promote wound
 CC healing. Ckalpha-2 antagonists can be used to treat rheumatoid
 CC arthritis, autoimmune and chronic and acute inflammatory and
 CC infective diseases, allergic reactions, prostaglandin-independent
 CC fever and bone marrow failure.

Sequence 99 AA;

Query Match 88.9%; Score 522; DB 18; Length 99;
 Best Local Similarity 99.0%; Pred. No. 6.7e-55;
 Matches 98; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 MRLIAAALLLLALYTAARDVDSKCKSRKGPRTIRYSDVKLEMKPRYPHCEKVIIT 72
 Db 1 mrliaaalllllalytarvdgskcksrkqklyrsvdkklemkpkypheekmvlitc 60

QY 73 KVSRYRGQEHCLHPKLOSTKRTIKWYNAMNEKRRVYEE 111

Db 61 kvsryrgqehclhpklgstkrfkikwynamnekrvryee 99

RESULT 9

AAV76089 standard; Protein; 95 AA.

AAV76089;

27-MAR-2000 (first entry)

Human CXC chemokine homologue huKSL, SEQ ID NO:344.

Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast;
 embryonic skin cell; keratinocyte stem cell; transit amplifying cell;
 secreted; transmembrane; inflammation; cancer; neurological disease;
 angiogenesis; tumour vascularisation; growth disorder;
 developmental disorder; skin wound; hair follicle disorder;
 anti-inflammatory; cyostatic; neuroprotective; vulnery.

Homo sapiens.

WO9955865-A1.

04-NOV-1999.

29-APR-1999; 99WO-NZ00051.

29-APR-1998; 98US-0069726.

09-NOV-1998; 98US-0188930.

PA (GENE-) GENESIS RES & DEV CORP LTD.
 XX Strachan L, Sleeman M, Watson JD, Onrust R, Kumble A, Murison JG;
 PI WPI: 2000-072177/06.
 XX DR N-PSDB; AAB61797.
 XX PT Novel polynucleotides useful for the treatment of various conditions
 XX including wounds and cancer -
 PS Claim 4: Page 202; 235pp; English.
 XX
 CC The invention relates to novel nucleic acid sequences derived from rat
 CC dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,
 CC and mouse embryonic skin, keratinocyte stem cells and transil amplifying
 CC cells. Polypeptides of the invention may be used to treat inflammation,
 CC cancer and neurological diseases. The proteins may be used to stimulate
 CC the growth and motility of keratinocytes, to inhibit the growth of
 CC cancer cells, to modulate angiogenesis and tumour vascularisation, to
 CC modulate skin inflammation, to modulate epithelial cell growth and to
 CC inhibit binding of HIV-1 to leukocytes. The invention may also be used
 CC to treat growth and developmental defects, skin wounds and hair follicle
 CC disorders. Sequences AAY75942-Y76123 represent polypeptides encoded
 CC by cDNA sequences derived from several mouse, rat or human skin cell
 CC types. Sequences AAY75942-Y75947, AAY76020-Y76021, AAY76094-Y76104 and
 CC AAY76119 are proteins with an N-terminal signal sequence, indicating
 CC that they are secreted. Sequences AAY75986-Y75989, AAY76061-Y76071,
 CC AAY76106-Y76109 and AAY76121-Y76122 are proteins with one or more
 CC putative transmembrane domains.
 XX
 SQ Sequence 95 AA:
 Query Match 86.7%; Score 509; DB 21; Length 95;
 Best Local Similarity 100.0%; Pred. No. 2e-51;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 17 AAILLLLLALTYARVDSKCKSRKGPRIKIRYSDVKLEMKRPYHCEKXVIITTKSVS 76
 DB 1 aaaillllllalytarvsgskcscrkpgkirygdvklmkpkyhceekmviitltsvsvs 60
 QY 77 RYRGDECHLPKLOSTKRFIKWYNANNEKRYVEE 111
 DB 61 ryrgehcilhpklqstkrifkwyawnekrvyee 95
 RESULT 10
 AAE05371
 ID AAE05371 standard; Protein; 95 AA.
 XX AC AAE05371;
 XX DT 12-SEP-2001 (first entry)
 XX DE Human hulk1 protein.
 XX KW Human; cytostatic; antiinflammatory; immunoregulatory; tissue integrity;
 KW wound healing; immune response; vaccine; cancer; asthma; allergy;
 KW cell trafficking; therapy; hulk1.
 XX OS Homo sapiens.
 XX PN WO200148192-A1.
 XX PD 05-JUL-2001.
 XX PF 21-DEC-2000; 2000WO-NZ00256.
 XX PR 23-DEC-1999; 99US-0171678.
 XX PR 28-NOV-2000; 2000US-0724864.
 XX PA (GENE-) GENESIS RES & DEV CORP LTD.
 XX

PI Watson JD, Murison JG;
 XX DR WPI: 2001-425665/45.
 XX DR N-PSDB; AAD10141.
 XX PT Novel isolated polypeptide useful to isolate corresponding interacting
 XX proteins or other compounds, to quantitatively determine levels of
 XX interacting proteins or other compounds, and as therapeutic target -
 PS Example 2: Page 94; 101pp; English.
 XX
 CC The patent discloses novel polynucleotides and their corresponding
 CC proteins which play a major role in induction of growth, cell migration
 CC and proliferation, cell-cell interaction and the differentiation of
 CC tissue-specific cells. These proteins are important in the maintenance
 CC of tissue integrity and thus are important in wound healing. They are
 CC useful in various assays to determine the biological activity, to raise
 CC antibodies, to isolate corresponding interacting proteins or other
 CC compounds, to quantitatively determine levels of interacting proteins or
 CC other compounds, and as therapeutic target in a whole range of disease
 CC states. Compositions comprising the novel proteins of the invention are
 CC useful for treating mammalian disorders. Polynucleotides of the invention
 CC are useful in genome and physical mapping, in positional cloning of
 CC genes, to tag or identify an organism or its reproductive material (as
 CC non-disruptive tags for marking organisms), and for the diagnosis and
 CC treatment of mammalian diseases which is the consequence of inappropriate
 CC expression of kinase genes. They are useful for promoting immune response
 CC as part of a vaccine or anti-cancer treatment, as target for cancer
 CC treatment, as immunoregulatory and anti-inflammatory molecule, as
 CC diagnostic for specific types of cancer and for development of an
 CC anti-cancer treatment, and as a target for antagonists in the treatment
 CC of diseases such as asthma and allergy. They are also useful to inhibit
 CC or enhance the activity of the soluble molecule that binds proteins of
 CC the invention, for tissue and neural regeneration, to promote or block
 CC cell trafficking, and as anti-inflammatory and/or vaccine adjuvant.
 CC The present sequence is human hulk1 protein.
 XX
 SQ Sequence 95 AA:
 Query Match 86.7%; Score 509; DB 22; Length 95;
 Best Local Similarity 100.0%; Pred. No. 2e-51;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 17 AAILLLLLALTYARVDSKCKSRKGPRIKIRYSDVKLEMKRPYHCEKXVIITTKSVS 76
 DB 1 aaaillllllalytarvsgskcscrkpgkirygdvklmkpkyhceekmviitltsvsvs 60
 QY 77 RYRGDECHLPKLOSTKRFIKWYNANNEKRYVEE 111
 DB 61 ryrgehcilhpklqstkrifkwyawnekrvyee 95
 RESULT 11
 AAB56028
 ID AAB56028 standard; Protein; 95 AA.
 XX AC AAB56028;
 XX DT 08-MAR-2001 (first entry)
 XX DE Skin cell protein, SEQ ID NO: 344.
 XX KW Human; skin cell; cytostatic; antiinflammatory; anti-HIV;
 KW neurotropic; neuroprotective; vulnerrary; immunomodulatory; vaccine;
 KW keratinocyte growth stimulation; cancer; angiogenesis inhibition;
 KW inflammation; neurological disease.
 XX OS Homo sapiens.
 XX PN WO200069884-A2.
 XX PD 23-NOV-2000.
 XX

XX 15-MAY-2000; 2000MO-N200075.
 PF
 XX 14-MAY-1999; 99US-0312283.
 PR
 XX (GENE-) GENESIS RES & DEV CORP LTD.
 PA
 XX Watson JD, Strachan L, Onrust R, Sleeman M, Kumble KD, Murison JG;
 PI WPI; 2001-007495/01.
 DR N-PSDB: AAC9730.
 DR
 XX New isolated polynucleotide used in the identification of genetic
 PT disorders and encoding polypeptides used for treating inflammatory
 PT disease, cancer and neurological diseases -
 XX
 PS Claim 4; Page 270; 352pp; English.
 PS
 XX The present sequence is a polypeptide which is expressed in
 CC mammalian skin cells. The polypeptide is useful for stimulating
 CC keratinocyte growth and motility, inhibiting the growth of cancer cells,
 CC modulating angiogenesis, inhibiting angiogenesis and vascularisation of
 CC tumours, modulating skin inflammation, stimulating the growth of
 CC epithelial cells, inhibiting the binding of human immunodeficiency virus
 CC (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and
 CC neurological diseases. The polynucleotide can be used as a marker, in
 CC the identification of genetic disorders, and for the design of
 CC oligonucleotides for examining expression patterns.
 CC
 SQ Sequence 95 AA:
 XX
 Query Match 86.7%; Score 509; DB 22; Length 95;
 Best Local Similarity 100.0%; Pred. No. 2e-51;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 17 AALLLLLLALYARVDSKCKSRGPKIRSYDVKKLEMKPKYPHCEKMYITTTKSVS 76
 DB 1 aaallllllalylarvdsckscsrkpkirysdvkklmkpkypkpcckmvylltksvs 60
 OY 77 RYRGQEHCHLPKIOSTKRFIKWYNAWNEKRYVEE 111
 DB 61 ryrqgchclhpklsqstkrflkwyawnekrivvee 95
 Db
 RESULT 12
 ID AAY31613 standard; Protein: 99 AA.
 XX
 AC AAY31613;
 XX
 DT 20-OCT-1999 (first entry)
 XX
 DE Murine neokine-1.
 XX
 KW Chemoattractant cytokine; chemokine; CXC motif; conserved cysteine;
 KW signal transduction modulation; angiogenesis inhibition;
 KW chemoattraction inhibition; cancer; inflammation; psoriasis;
 KW post-transplantation organ rejection.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..22
 FT /label= Signal_peptide
 FT Protein 23..99
 FT /note= "Murine mature neokine-1"
 FT Region 25..72
 FT /label= CXC_motif
 FT /note= "Conserved Cys at 25, 27, 51 and 72"
 XX
 PN MO9940104-AL.
 XX

PD 12-AUG-1999.
 XX
 PF 10-FEB-1999; 99WO-US02943.
 XX
 PR 10-FEB-1998; 98US-0023664.
 XX
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 XX
 PI Barnes TM, Mackay C;
 DR WPI; 1999-494271/41.
 DR N-PSDB: AA208963.
 DR
 XX Novel neokine polypeptides and polynucleotides used for regulating
 PT and treating proliferative disorders and diseases
 PT
 XX
 PS Claim 1; Fig 2; 123pp; English.
 PS
 XX This sequence represents murine neokine-1. The neokines are a novel
 CC family of chemoattractant cytokines (chemokines) and are ligands for a
 CC previously identified putative G protein-coupled receptor termed RDC1
 CC (also called the neokine receptor). The neokines are members of the
 CC non-ELR-CXC subfamily of chemokines characterised by the absence of an
 CC ELR motif and the presence of a CXC signature motif. The CXC motif
 CC encompasses 4 highly conserved cysteine residues, with the first two
 CC cysteines separated by one non-conserved amino acid residue; however,
 CC the neokines show some atypical features which distinguish them from
 CC previously characterised CXC chemokines e.g., the presence of
 CC approximately 5 residues between the third and fourth conserved
 CC cysteines. The neokines have a variety of functions, including
 CC modulation of signal transduction, inhibition of angiogenesis,
 CC regulation of inflammation and inhibition of chemoattraction.
 CC Neokines may therefore be useful in the treatment of various
 CC proliferative disorders or diseases; several types of cancer,
 CC inflammation, psoriasis, and immune rejection following skin graft
 CC and kidney transplantation. Neokines, their associated polynucleotides,
 CC homologues and antibodies can be used in screening for drugs or
 CC compounds which modulate their activity and therefore may be important
 CC for the development of new therapeutics.
 CC
 SQ Sequence 99 AA:
 XX
 Query Match 86.2%; Score 506; DB 20; Length 99;
 Best Local Similarity 94.9%; Pred. No. 4.7e-51;
 Matches 94; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 OY 13 MRLAALLLLALYARVDSKCKSRGPKIRSYDVKKLEMKPKYPHCEKMYITTT 72
 DB 1 mrlaalllllalcasrvdsgskscsrkpkirysdvkklmkpkypkpcckmvyllt 60
 OY 73 KVSRYRGQEHCHLPKIOSTKRFIKWYNAWNEKRYVEE 111
 DB 61 kmsrtyrgqchclhpklsqstkrflkwyawnekrivvee 99
 Db
 RESULT 13
 ID AAY76085 standard; Protein: 99 AA.
 XX
 AC AAY76085;
 XX
 DT 27-MAR-2000 (first entry)
 XX
 DE Murine CXC chemokine homologue mUKSL, SEQ ID NO:340.
 XX
 KW skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast;
 KW embryonic skin cell; keratinocyte stem cell; transient amplifying cell;
 KW secreted; transmembrane; inflammation; cancer; neurological disease;
 KW angiogenesis; tumour vascularisation; growth disorder;
 KW developmental disorder; skin wound; hair follicle disorder;
 KW anti-inflammatory; cytostatic; neuroprotective; vulnery.
 XX

OS Mus sp.
 XX WO9955865-A1.
 XX
 XX PD 04-NOV-1999.
 XX
 XX PF 29-APR-1999; 99WO-NZ00051.
 XX
 XX PR 29-APR-1998; 98US-0069726.
 XX PR 09-NOV-1998; 98US-0188930.
 XX PA (GENE-) GENESIS RES & DEV CORP LTD.
 XX
 XX PI Strachan L, Sleeman M, Watson JD, Orrust R, Kumble A, Morrison JG;
 XX WPI: 2000-072177/06.
 XX DR N-PSDB; AA261790.
 XX
 XX PT Novel polynucleotides useful for the treatment of various conditions
 XX including wounds and cancer -
 XX
 XX PS Claim 4; Page 200; 235pp; English.
 CC The invention relates to novel nucleic acid sequences derived from rat
 CC dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,
 CC and mouse embryonic skin, keratinocyte stem cells and transit amplifying
 CC cells. Polypeptides of the invention may be used to treat inflammation,
 CC cancer and neurological diseases. The proteins may be used to stimulate
 CC the growth and motility of keratinocytes, to inhibit the growth of
 CC cancer cells, to modulate angiogenesis and tumour vascularisation, to
 CC modulate skin inflammation, to modulate epithelial cell growth and to
 CC inhibit binding of HIV-1 to leukocytes. The invention may also be used
 CC to treat growth and developmental defects, skin wounds and hair follicle
 CC disorders. Sequences AAY75942-Y76123 represent polypeptides encoded
 CC by cDNA sequences derived from several mouse, rat or human skin cell
 CC types. Sequences AAY75942-Y75947, AAY76020-Y76021, AAY76094-Y76104 and
 CC AAY76119 are proteins with an N-terminal signal sequence, indicating
 CC that they are secreted. Sequences AAY75986-Y75989, AAY76061-Y76071,
 CC AAY76106-Y76109 and AAY76121-Y76122 are proteins with one or more
 CC putative transmembrane domains.
 CC
 XX Sequence 99 AA;
 SO

Query Match 86.2%; Score 506; DB 21; Length 99;
 Best Local Similarity 94.9%; Pred. No. 4.7e-51;
 Matches 94; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 13 MRLAALLLLLALYARVDSKCSKSRGPKIRYSDVKLEMPKYPHCEKMTITT 72
 |||
 Db 1 mrlaaallllllalcastrvgskckscrkpgklyrsdvkklmmpkypheekmviytl 60

OY 73 KSVSRVGOEHCHPRLQSTKRIRKYNWANEKRRYEE 111
 |||
 Db 61 kmsryrgchclhpklgsktkrikynawnekriryee 99

RESULT 14
 AAY76115
 ID AAY76115 standard; Protein; 99 AA.
 XX
 XX AC AAY76115;
 XX
 XX DT 27-MAR-2000 (first entry)
 XX
 XX DE Full-length murine CXCL chemokine homologue muKSL, SEQ ID NO:394.
 XX
 XX SKIN; dermal papilla; keratinocyte; neonatal foreskin fibroblast;
 KW embryonic skin cell; keratinocyte stem cell; transit amplifying cell;
 KW secreted; transmembrane; inflammation; cancer; neurological disease;
 KW angiogenesis; tumour vascularisation; growth disorder;
 KW developmental disorder; skin wound; hair follicle disorder;
 KW anti-inflammatory; cytostatic; neuroprotective; vulnery.

XX
 OS Mus sp.
 XX WO9955865-A1.
 XX
 XX PD 04-NOV-1999.
 XX
 XX PF 29-APR-1999; 99WO-NZ00051.
 XX
 XX PR 29-APR-1998; 98US-0069726.
 XX PR 09-NOV-1998; 98US-0188930.
 XX PA (GENE-) GENESIS RES & DEV CORP LTD.
 XX
 XX PI Strachan L, Sleeman M, Watson JD, Orrust R, Kumble A, Morrison JG;
 XX WPI: 2000-072177/06.
 XX DR N-PSDB; AA261823.
 XX
 XX PT Novel polynucleotides useful for the treatment of various conditions
 XX including wounds and cancer -
 XX
 XX PS Claim 4; Page 223; 235pp; English.
 CC The invention relates to novel nucleic acid sequences derived from rat
 CC dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,
 CC and mouse embryonic skin, keratinocyte stem cells and transit amplifying
 CC cells. Polypeptides of the invention may be used to treat inflammation,
 CC cancer and neurological diseases. The proteins may be used to stimulate
 CC the growth and motility of keratinocytes, to inhibit the growth of
 CC cancer cells, to modulate angiogenesis and tumour vascularisation, to
 CC modulate skin inflammation, to modulate epithelial cell growth and to
 CC inhibit binding of HIV-1 to leukocytes. The invention may also be used
 CC to treat growth and developmental defects, skin wounds and hair follicle
 CC disorders. Sequences AAY75942-Y76123 represent polypeptides encoded
 CC by cDNA sequences derived from several mouse, rat or human skin cell
 CC types. Sequences AAY75942-Y75947, AAY76020-Y76021, AAY76094-Y76104 and
 CC AAY76119 are proteins with an N-terminal signal sequence, indicating
 CC that they are secreted. Sequences AAY75986-Y75989, AAY76061-Y76071,
 CC AAY76106-Y76109 and AAY76121-Y76122 are proteins with one or more
 CC putative transmembrane domains.
 CC
 XX Sequence 99 AA;
 SO

Query Match 86.2%; Score 506; DB 21; Length 99;
 Best Local Similarity 94.9%; Pred. No. 4.7e-51;
 Matches 94; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 13 MRLAALLLLLALYARVDSKCSKSRGPKIRYSDVKLEMPKYPHCEKMTITT 72
 |||
 Db 1 mrlaaallllllalcastrvgskckscrkpgklyrsdvkklmmpkypheekmviytl 60

OY 73 KSVSRVGOEHCHPRLQSTKRIRKYNWANEKRRYEE 111
 |||
 Db 61 kmsryrgchclhpklgsktkrikynawnekriryee 99

RESULT 15
 AAB56024
 ID AAB56024 standard; Protein; 99 AA.
 XX
 XX AC AAB56024;
 XX
 XX DT 08-MAR-2001 (first entry)
 XX
 XX DE Skin cell protein, SEQ ID NO: 340.
 XX
 XX SKIN cell
 KW Mouse; skin cell; cytostatic; anti-inflammatory; anti-HIV;
 KW neurotrophic; neuroprotective; vulnery; immunomodulatory; vaccine;
 KW keratinocyte growth stimulation; cancer; angiogenesis inhibition;
 KW inflammation; neurological disease.

05 Mus sp.

PN WO2000069884-A2

PD 23-NOV-2000.

PF 15-MAY-2000; 2000WO-NZ00075.

PR 14-MAY-1999; 99US-0312283

PA (GENE-) GENESIS RES & DEV CORP LTD.

PI Watson JD, Strachan L, Onrust R, Sleeman M, Kumble KD, Morrison JG,

DR WPI; 2001-007495/01

XX DE AGO 1967

PT New isolated polynucleotide used in the identification of genetic disorders and encoding polypeptides used for treating inflammatory disease, cancer and neurological diseases -

PS Claim 4; Page 268; 352pp; English.

The present sequence is a polypeptide which is expressed in mammalian skin cells. The polypeptide is useful for stimulating keratinocyte growth and motility, inhibiting the growth of cancer cells, modulating angiogenesis, inhibiting angiogenesis and vascularisation of tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of human immunodeficiency virus (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of oligonucleotides for examining expression patterns.

5Q Sequence 99 AA;

Query Match	Score	DB	Length
86.2%	506	22	99

Matches	94;	Conservative	3;	Mismatches	4;
---------	-----	--------------	----	------------	----

13 MRLAALLLLLTARVDGSKCKSRKGPKIRYSDVKKLEMKPKYPHCEEKVIIT 72

Db 1 mr1laa11111alcastrvdgskckcsrkqpkirysdvkklcmkpkypnccekmvltt bu

73 KSVSRYRGQEHCLHPKLQSTKRFIKWYNANNEKRRVYEE 111

Db 61 ksmstrygqehclhpk1gstkrflkwynawnekrivyee 99

Search completed: January 29, 2002, 16:04:06
Job time: 32 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 29, 2002, 16:03:34 ; Search time 12.49 Seconds
(without alignments)
199,989 Million cell updates/sec

Title: US-09-978-189-370

Perfect score: 587
Sequence: 1 MSLLPRRAPVSMRLAAAL.....TKRFIKYNAWNEKRYVEE 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: Issued_Patents_AA:*
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4: /cgn2_6/prodata/2/1aa/6A.COMB.pep:*
5: /cgn2_6/prodata/2/1aa/6B.COMB.pep:*
6: /cgn2_6/prodata/2/1aa/PCRTUS.COMB.pep:*
7: /cgn2_6/prodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	582	99.1	111	2	US-08-825-556A-2
2	522	88.9	99	4	US-08-825-556A-3
3	509	86.7	95	4	US-09-188-930-344
4	506	86.2	99	4	US-09-188-930-340
5	428	72.9	77	4	US-09-188-930-346
6	424	72.2	77	4	US-09-188-930-345
7	298	50.8	133	4	US-09-188-930-157
8	143.5	24.4	98	2	US-08-825-556A-4
9	143.5	24.4	100	4	US-08-679-492A-146
10	138	23.5	100	3	US-08-476-376-2
11	128.5	21.9	107	1	US-08-352-324A-4
12	128.5	21.9	107	2	US-08-862-607-4
13	128.5	21.9	107	2	US-08-468-819-6
14	128.5	21.9	107	2	US-09-203-235-4
15	128.5	21.9	107	5	PCT-US95-16144-4
16	117.5	20.0	107	1	US-08-352-324A-7
17	117.5	20.0	107	2	US-08-862-607-7
18	117.5	20.0	107	2	US-08-468-819-5
19	117.5	20.0	107	3	US-09-203-235-7
20	117.5	20.0	107	5	PCT-US95-16144-7
21	113	19.3	71	2	US-08-812-003-9
22	109	18.6	106	4	US-08-679-493A-148
23	107	18.2	106	1	US-08-352-324A-5
24	107	18.2	106	2	US-08-862-607-5
25	107	18.2	106	3	US-08-468-819-7
26	107	18.2	106	3	US-09-203-235-5
27	107	18.2	106	5	PCT-US95-16144-5

28	99.5	17.0	73	2	US-08-436-420-42	Sequence 42, Appl
29	99.5	17.0	74	3	US-08-476-376-3	Sequence 3, Appl1
30	97	16.5	96	4	US-08-679-493A-147	Sequence 147, App
31	95.5	16.3	78	2	US-08-436-420-38	Sequence 38, Appl
32	94.5	16.1	126	1	US-07-624-742-1	Sequence 1, Appl1
33	93.5	15.9	77	2	US-08-436-420-39	Sequence 39, Appl
34	89.5	15.2	72	2	US-08-436-420-43	Sequence 43, Appl
35	88.5	15.1	72	3	US-08-846-966-1	Sequence 1, Appl1
36	88.5	15.1	72	3	US-08-557-142-1	Sequence 1, Appl1
37	88.5	15.1	72	5	PCT-US94-06264-1	Sequence 41, Appl1
38	88.5	15.1	77	2	US-08-436-420-41	Sequence 41, Appl
39	88	15.0	101	5	PCT-US95-16144-8	Sequence 8, Appl1
40	87.5	14.9	73	1	US-07-792-988-3	Sequence 3, Appl1
41	87.5	14.9	73	1	US-07-778-413E-19	Sequence 19, Appl
42	87.5	14.9	73	1	US-08-340-102-19	Sequence 19, Appl
43	87.5	14.9	73	2	US-08-436-420-27	Sequence 27, Appl
44	87.5	14.9	73	3	US-08-846-966-3	Sequence 3, Appl1
45	87.5	14.9	73	5	PCT-US94-06264-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-08-825-556A-2
; Sequence 2, Application US/08825556A
; Patent No. 5910431
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Su, Jeffrey Y.
; APPLICANT: Li, Haodong
; TITLE OF INVENTION: Chemokine Alpha 2
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-2934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,556A
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,653
; FILING DATE: 19-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488, 0850001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-825-556A-2

Query Match 99.1%; Score 582; DB 2; Length 111;
Best Local Similarity 99.1%; Pred. No. 8.6e-64;
Matches 110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSLLPRAPVSMRLAALLLLLLALTYARVDGSKCKSRKGPRIKIRYSDVKKLEMKPKY 60
 DB 1 MSLLPRAPVSMRLAALLLLLLALTYARVDGSKCKSRKGPRIKIRYSDVKKLEMKPKY 60
 QY 61 PHCEKVVITTKSVSRVSGOEHCHLPKLOSTKRFIKWYNNANNEKRRVYEE 111
 DB 61 PHCEKVVITTKSVSRVSGOEHCHLPKLOSTKRFIKWYNNANNEKRRVYEE 111

RESULT 2

US-08-825-556A-3
 ; Sequence 3, Application US/08825556A
 ; Patent No. 5910431
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni, Jian
 ; APPLICANT: Gentz, Reinert L.
 ; APPLICANT: Su, Jeffrey Y.
 ; APPLICANT: Li, Haodong
 ; TITLE OF INVENTION: Chemokine Alpha 2
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
 ; STREET: 1100 New York Ave., Suite 600
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-2934
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/825,556A
 ; FILING DATE: 19-MAR-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/013,653
 ; FILING DATE: 19-MAR-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Steffe, Eric K.
 ; REGISTRATION NUMBER: 36,688
 ; REFERENCE/DOCKET NUMBER: 1488.0850001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-371-2600
 ; TELEFAX: 202-371-2540
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 99 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-825-556A-3

Query Match 88.9%; Score 522; DB 2; Length 99;
 Best Local Similarity 99.0%; Pred. No. 1.6e-56;
 Matches 98; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 MRLIAALLLLLLALTYARVDGSKCKSRKGPRIKIRYSDVKKLEMKPKYPHCEKVVITTT 72
 DB 1 MRLIAALLLLLLALTYARVDGSKCKSRKGPRIKIRYSDVKKLEMKPKYPHCEKVVITTT 60
 QY 73 KVSRYRGOEHCHLPKLOSTKRFIKWYNNANNEKRRVYEE 111
 DB 61 KVSRYRGOEHCHLPKLOSTKRFIKWYNNANNEKRRVYEE 99

RESULT 3

US-09-188-930-344
 ; Sequence 344, Application US/09188930A
 ; Patent No. 6150502
 ; GENERAL INFORMATION:

; APPLICANT: Watson, James D.
 ; APPLICANT: Strachan, Lorna
 ; APPLICANT: Sleeman, Matthew
 ; APPLICANT: Onrust, Rene
 ; APPLICANT: Murison, James Greg
 ; TITLE OF INVENTION: Compositions Isolated From Skin Cells
 ; FILE REFERENCE: 11000.1011cl
 ; CURRENT APPLICATION NUMBER: US/09/188,930A
 ; CURRENT FILING DATE: 1998-11-09
 ; NUMBER OF SEQ ID NOS: 348
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 344
 ; LENGTH: 95
 ; TYPE: PRT
 ; ORGANISM: Mouse
 ; US-09-188-930-344

Query Match 86.7%; Score 509; DB 4; Length 95;
 Best Local Similarity 100.0%; Pred. No. 5.8e-55;
 Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 AALLLLLLALTYARVDGSKCKSRKGPRIKIRYSDVKKLEMKPKYPHCEKVVITTKSVS 76
 DB 1 AALLLLLLALTYARVDGSKCKSRKGPRIKIRYSDVKKLEMKPKYPHCEKVVITTKSVS 60
 QY 77 RYRGOEHCHLPKLOSTKRFIKWYNNANNEKRRVYEE 111
 DB 61 RYRGOEHCHLPKLOSTKRFIKWYNNANNEKRRVYEE 95

RESULT 4

US-09-188-930-340
 ; Sequence 340, Application US/09188930A
 ; Patent No. 6150502
 ; GENERAL INFORMATION:
 ; APPLICANT: Watson, James D.
 ; APPLICANT: Strachan, Lorna
 ; APPLICANT: Sleeman, Matthew
 ; APPLICANT: Onrust, Rene
 ; APPLICANT: Murison, James Greg
 ; TITLE OF INVENTION: Compositions Isolated From Skin Cells
 ; FILE REFERENCE: 11000.1011cl
 ; CURRENT APPLICATION NUMBER: US/09/188,930A
 ; CURRENT FILING DATE: 1998-11-09
 ; NUMBER OF SEQ ID NOS: 348
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 340
 ; LENGTH: 99
 ; TYPE: PRT
 ; ORGANISM: Mouse
 ; US-09-188-930-340

Query Match 86.2%; Score 506; DB 4; Length 99;
 Best Local Similarity 94.9%; Pred. No. 1.4e-54;
 Matches 94; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 13 MRLIAALLLLLLALTYARVDGSKCKSRKGPRIKIRYSDVKKLEMKPKYPHCEKVVITTT 72
 DB 1 MRLIAALLLLLLALTYARVDGSKCKSRKGPRIKIRYSDVKKLEMKPKYPHCEKVVITTT 60
 QY 73 KVSRYRGOEHCHLPKLOSTKRFIKWYNNANNEKRRVYEE 111
 DB 61 KVSRYRGOEHCHLPKLOSTKRFIKWYNNANNEKRRVYEE 99

RESULT 5

US-09-188-930-346
 ; Sequence 346, Application US/09188930A
 ; Patent No. 6150502

RESULT 7
US-09-188-930-157
; Sequence 157, Application US/091889301

RESULT 8
 US-08-825-556A-4
 Sequence 4, Application US/08825556A
 Patent No. 5910431
 GENERAL INFORMATION:
 APPLICANT: Ni, Jian
 APPLICANT: Gentz, Reiner L.
 APPLICANT: Su, Jeffrey Y.
 APPLICANT: Li, Haodong
 TITLE OR INVENTION: Chemokine Alpha 2
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
 STREET: 1100 New York Ave., Suite 600
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005-2934
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/825,556A
 FILING DATE: 19-MAR-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/013,653
 FILING DATE: 19-MAR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Steffe, Eric K.
 REGISTRATION NUMBER: 36,688
 REFERENCE/DOCKET NUMBER: 1488.0850001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEO ID NO: 4:
 SEQUENCE CHARACTERISTICS:

```

; STREET: 411 HACKENSACK AVE, CONTINENTAL PLAZA, 4TH
; STREET: STREET:
; FLOOR

```

ANTI-SENSE: NO
-476-376-2

62 HCEKMWITTKSVSRYYRGQEHCLHPKLOSTKRFIK 97

ADDRESS:	Incyte Pharmaceuticals, Inc.	21.9%;	Score 128.5;	DB 2;	Length 107;
STREET:	3174 Porter Drive	Best Local	Similarity 33.3%;	Pred. No. 2e-08;	
CITY:	Palo Alto	Matches 42;	Conservative 18;	Mismatches 35;	Indels 11; Gaps 2.
STATE:	CA				
COUNTRY:	US				
ZIP:	94304				
COMPUTER READABLE FORM:					
MEDIUM TYPE:	Diskette				
COMPUTER:	IBM Compatible				
OPERATING SYSTEM:	DOS				
SOFTWARE:	FastSeq Version 1.5				
CURRENT APPLICATION DATA:					
APPLICATION NUMBER:	US/08/862,607				
FILING DATE:	23-MAY-1997				
CLASSIFICATION:	435				
PRIOR APPLICATION DATA:					
APPLICATION NUMBER:	08/352,324				
FILING DATE:	07-DEC-1994				
ATTORNEY/AGENT INFORMATION:					
NAME:	Luther, Barbara J.				
REGISTRATION NUMBER:	33,954				
REFERENCE/DOCKET NUMBER:	PF-0025 US				
TELECOMMUNICATION INFORMATION:					
TELEPHONE:	415-855-0555				
TELEFAX:	415-852-0195				
INFORMATION FOR SEQ ID NO: 4:					
SEQUENCE CHARACTERISTICS:					
LENGTH:	107 amino acids				
TYPE:	amino acid				
STRANDEDNESS:	single				
TOPOLOGY:	linear				
MOLECULE TYPE:	peptide				
US-08-862-607-4					
Query Match					
Best Local					
Matches					
QY	8 APYVSMKLAALALLLALTYRVDG-----KCKCSRGRPKIRYSDYKLEMPKYP 61				
DB	8 AANSNRLRLVALLLLLVASRRAGAPLATELRCQCLQTLGSHLNKNIGSVKVSPPG 67				
QY	62 HCEKNVIITTKSVSRKRGQEHCLHPKIQSTKRFK 97				
DB	68 HCAQTEVIATIKN----GQKACLNPASPWKIIE 98				
RESULT 13					
US-08-468-819-6					
Sequence 6,	Application US/08468819				
Patent No.	15871723				
GENERAL INFORMATION:					
APPLICANT:	Strieter, Robert M.				
APPLICANT:	Polverini, Peter J.				
APPLICANT:	Kunkel, Steven L.				
TITLE OF INVENTION:	CXC Chemokines as Regulators of				
TITLE OF INVENTION:	Angiogenesis				
NUMBER OF SEQUENCES:	93				
CORRESPONDENCE ADDRESS:					
ADDRESSEE:	Arnold, White & Durkee				
STREET:	P.O. Box 4433				
CITY:	Houston				
STATE:	TX				
COUNTRY:	US				
ZIP:	77210				
COMPUTER READABLE FORM:					
MEDIUM TYPE:	Floppy disk				
COMPUTER:	IBM PC compatible				
OPERATING SYSTEM:	PC-DOS/MS-DOS				
SOFTWARE:	Patent Release #1.0, Version #1.30				
CURRENT APPLICATION DATA:					
APPLICATION NUMBER:	US/08/468,819				

FILED DATE: Concurrently herewith
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UMIC.003/HVL
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7477
TELEX: N/A
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-468-819-6

Query Match 21.9%; Score 128.5; DB 2; Length 107;
Best Local Similarity 33.3%; Pred. No. 2e-08;
Matches 32; Conservative 18; Mismatches 35; Indels 11; Gaps 2;

QY 8 APPVSMRLAAALLLLALTYTARVDG-----KCKSRKGPRIKRYSDVKLEMKPKYP 61
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DB 8 AAPSRLRLRVALLLLLVASRAAGAPLATELRCCCLTQLOGIHLNKIOSVVKSGP 67
| : ||| ||||| : | : : : : |

QY 62 HCEEKVITTKSVSRGQEHCLHPKLOSTRKRIK 97
| : ||| ||||| : | : : : : |
DB 68 HCAQTEVIATLKN-----GQKACLNPA SPVWKIIE 98
| : ||| ||||| : | : : : : |

RESULT 14
US-09-203-235-4
Sequence 4, Application US/09203235
Patent No. 6071701
GENERAL INFORMATION:
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Wilde, Craig G.
APPLICANT: Seilheimer, Jeffrey J.
TITLE OF INVENTION: A NOVEL CHEMOKINE EXPRESSED IN
TITLE OF INVENTION: INFLAMED ADENOID, ITS PRODUCTION AND USES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/203,235
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/862,607
FILING DATE: 23-MAY-1997
APPLICATION NUMBER: 08/352,324
FILING DATE: 07-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0025 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-203-235-4

Query Match 21.9%; Score 128.5; DB 3; Length 107;
Best Local Similarity 33.3%; Pred. No. 2e-08;
Matches 32; Conservative 18; Mismatches 35; Indels 11; Gaps 2;

QY 8 APPVSMRLAAALLLLALTYTARVDG-----KCKSRKGPRIKRYSDVKLEMKPKYP 61
| : ||| ||||| : | : : : : |
DB 8 AAPSRLRLRVALLLLLVASRAAGAPLATELRCCCLTQLOGIHLNKIOSVVKSGP 67
| : ||| ||||| : | : : : : |

QY 62 HCEEKVITTKSVSRGQEHCLHPKLOSTRKRIK 97
| : ||| ||||| : | : : : : |
DB 68 HCAQTEVIATLKN-----GQKACLNPA SPVWKIIE 98
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RESULT 15
PCT-US95-16144-4
Sequence 4, Application PC/TUS9516144
GENERAL INFORMATION:
APPLICANT: INCYTE PHARMACEUTICALS, INC.
TITLE OF INVENTION: A NOVEL CHEMOKINE EXPRESSED IN INFLAMED
TITLE OF INVENTION: ADENOID, ITS PRODUCTION AND USES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16144
FILING DATE: 07-DEC-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,324
FILING DATE: 07-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: LUTHER, BARBARA J.
REGISTRATION NUMBER: 33954
REFERENCE/DOCKET NUMBER: PF-0025 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-16144-4

Query Match 21.9%; Score 128.5; DB 5; Length 107;
Best Local Similarity 33.3%; Pred. No. 2e-08;
Matches 32; Conservative 18; Mismatches 35; Indels 11; Gaps 2;

QY 8 APPVSMRLAAALLLLALTYTARVDG-----KCKSRKGPRIKRYSDVKLEMKPKYP 61
| : ||| ||||| : | : : : : |

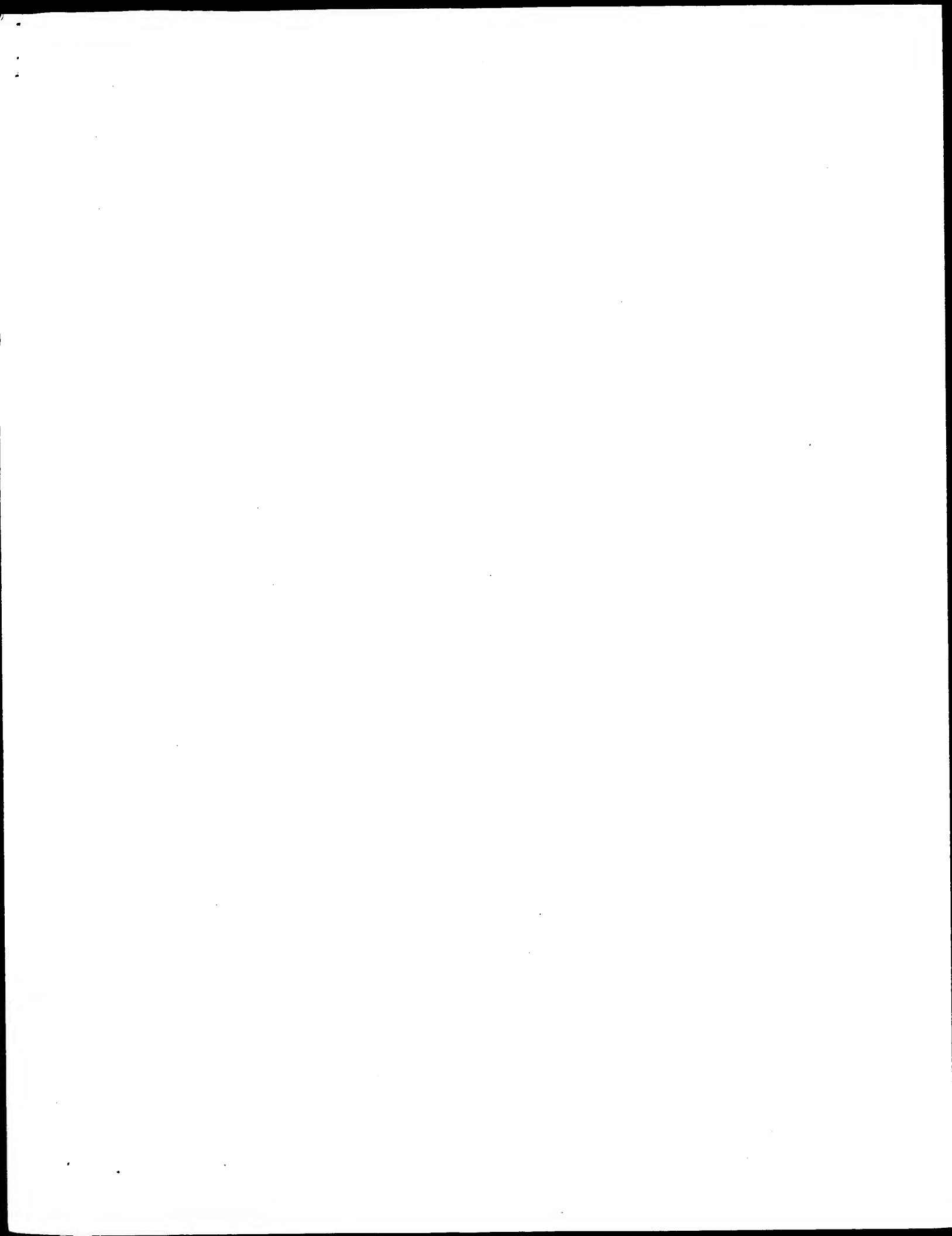
Wed Jan 30 09:49:25 2002

us-09-978-189-370.ra1

Page 7

D_b 8 AAPSNPPLTEVALLLLLLLVASRSRAGAPLATEIRCOCLQTLOGIH.KNIQSVKVKSPGP 67
Q_Y 62 HCEKMVIITTSKVSRYRGQEHLCHKPKIQTSTKRPIK 97
 || : || | : || : || : | | : :
D_b 68 HCAQTVEIATLN-----GQRKLNPASPMPKKIIIE 98

Search completed: January 29, 2002, 16:04:25
Job time: 51 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 29, 2002, 16:03:34 ; Search time 14.34 Seconds

(without alignments)
589,636 Million cell updates/sec

Title: US-09-978-189-370

Perfect score: 1 MSLLPRAPPVSMRLAAL.....TKRFIKYNAWNEKRYVEE 111

Sequence: 1 MSLLPRAPPVSMRLAAL.....TKRFIKYNAWNEKRYVEE 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	520	88.6	99	2 JG0182	chemokine BRK - h
2	143.5	24.4	100	2 S46198	cytokine-induced n
3	138	23.5	100	2 JH0200	macrophage inflam
4	131	22.3	101	2 B28414	growth-regulated p
5	128.5	21.9	107	2 JH0281	macrophage inflam
6	124	21.1	100	2 S21467	macrophage inflam
7	117.5	20.0	107	2 A28414	macrophage inflam
8	116.5	19.8	107	2 B38290	macrophage inflam
9	116.5	19.8	107	2 B38290	macrophage inflam
10	111	18.9	96	2 A32954	gro-alpha precurs
11	103	17.5	117	2 B44253	alveolar macroph
12	97	16.5	96	2 JN0572	neutrophil chemo-a
13	94.5	16.1	126	2 A35766	platelet factor 4
14	87.5	14.9	125	2 JN0470	interferon gamma-1
15	85.5	14.6	53	2 I51886	macrophage inflam
16	84	14.3	104	1 PFH04A	macrophage inflam
17	82.5	14.1	103	2 A53096	platelet factor 4
18	82.5	14.1	128	1 TGHU	interleukin-8 prec
19	81.5	13.9	95	2 JN0841	beta-thromboglobul
20	81	13.8	101	1 PFH04	interleukin-8 - do
21	80.5	13.7	53	2 I64831	platelet factor 4
22	80.5	13.7	98	2 A45492	gene KC protein -
23	80.5	13.7	103	2 A26736	IP-10 precursor -
24	80.5	13.7	103	2 I50417	transformation-ind
25	80	13.6	119	2 S42881	RSV-induced protei
26	79.5	13.5	98	1 TGHUG1	platelet basic pro
27	79.5	13.5	101	2 S42496	interferon gamma-1
28	76.5	13.0	114	2 A55010	interleukin-8 prec
29	76	12.9	132	2 A57325	neutrophil-activat
					C-X-C chemokine LI

30	75	12.9	677	2 T27127	hypothetical prote
31	74	12.6	394	2 T32670	hypothetical prote
32	73.5	12.5	75	2 A54188	granulocyte chemot
33	73	12.4	105	2 A26774	platelet factor 4
34	72.5	12.4	101	2 I46871	interleukin-8 - ra
35	71.5	12.2	75	2 B54188	granulocyte chemot
36	71	12.1	99	2 A37034	interleukin-8 prec
37	71	12.1	1270	2 T28087	hypothetical prote
38	70	11.9	308	1 S76941	carbamate kinase (
39	69.5	11.8	98	2 I59277	hypothetical prote
40	69.5	11.8	807	1 I51685	replication licens
41	68	11.6	149	2 T25246	hypothetical prote
42	68	11.6	309	2 S76393	hypothetical prote
43	68	11.6	581	2 C84251	flagella accessory
44	67.5	11.5	90	2 S69133	platelet factor 4
45	67	11.4	647	2 JEO337	frizzled-1 protein

ALIGNMENTS

RESULT 1
JG0182
chemokine BRK - human
C:Species: Homo sapiens (man)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 11-May-2000
C:Accession: JG0182
R:Hromas, R.; Broxmeyer, H.E.; Kim, C.; Nakshatri, H.; Christopherson II, K.; Hou, Y.
Biochem. Biophys. Res. Commun. 255, 703-706, 1999
A>Title: Cloning of BRK, a novel divergent CXC chemokine preferentially expressed in
A:Reference number: JG0182; MUID:99160416
A:Accession: JG0182
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-99 <HRO>
A:Cross-references: CB:AF073957
C:Superfamily: beta-thromboglobulin

Query Match 88.6%; Score 520; DB 2; Length 99;
Best Local Similarity 99.0%; Pred. No. 3.2e-47;
Matches 98; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 MRLAALLLLLLALYARVDGSKCKSRKGPRIYSDVKLEMKPKYPHCEKWIIT 72
DB 1 MRLPAALLLLLLALYARVDGSKCKSRKGPRIYSDVKLEMKPKYPHCEKWIIT 60
QY 73 KSVSRVKGQEHCLHPKLOSTKRFIKYNAWNEKRYVEE 111
DB 61 KSVSRVKGQEHCLHPKLOSTKRFIKYNAWNEKRYVEE 99

RESULT 2
S46198
cytokine-induced neutrophil chemoattractant 2 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C:Accession: S46198; C48988
R:Nakagawa, H.; Komorita, N.; Shibata, F.; Ikese, A.; Konishi, K.; Fujio, M.; Kato
Biochem. J. 301, 545-550, 1994
A>Title: Identification of cytokine-induced neutrophil chemoattractants (CINC), rat G
ences and characterization.
A:Reference number: S46198; MUID:94318061
A:Accession: S46198
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-100 <NAK>
A:Cross-references: EMBL:D21095; NID:G517143; PIDN:BA04657.1; PID:G517144
R:Nakagawa, H.; Ikese, A.; Hatakeyama, S.; Kato, H.; Gotoda, T.; Komorita, N.; Watan
Biochem. Pharmacol. 45, 1425-1430, 1993
A>Title: Production of an interleukin-8-like chemokine by cytokine-stimulated rat NRK
A:Reference number: A48988; MUID:93228656
A:Accession: C48988

OY 62 HCEKMWITTKSVSRVGOEHCLHPKLOSTKREIK 97
 Db 68 HCAQTEVIATLKND-----GQKACLNPPASPMVKRIIE 98

RESULT 6

S21467
 macrophage inflammatory protein 2 - rat
 N:Alternate names: chemoattractant P-1
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Aug-1999
 C:Accession: S21467; D48988
 R:Discoll, K.
 Submitted to the EMBL Data Library, April 1992
 A:Reference number: S21467
 A:Accession: S21467
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-100 <DR1>
 A:Cross-references: EMBL:X65647; NID:956665; PIDN:CAA46599.1; PID:956666
 R:Nakagawa, H.; Ikeue, A.; Hatakeyama, S.; Kato, H.; Gotoda, T.; Komorita, N.; Watanabe
 Biochem. Pharmacol. 45, 1425-1430, 1993
 A:Title: Production of an interleukin-8-like chemokine by cytokine-stimulated rat NRK-49
 A:Reference number: A48988; MUID:93228656
 A:Accession: D48988
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 32-45 <NAK>
 A:Experimental source: kidney, NRK-49F fibroblasts
 A:Note: sequence extracted from NCBI backbone (NCBIP:129129)
 C:Superfamily: beta-thromboglobulin

Query Match 21.1%; Score 124; DB 2; Length 100;
 Best local similarity 33.7%; Pred. No. 6.3e-06;

Matches 32; Conservative 16; Mismatches 37; Indels 10; Gaps 3;

OY 8 APPVSRMLAALALLLLALY---TARVDS--KCKCRKRPKIRYSDVKLEMKPKYPH 62
 Db 2 APPTRQLNNAVILVLLLLATNHHOGTGVVVAASELRQCILTLTPRVDFKNIQSLTVTPPGPH 61
 OY 63 CEEKMWITTKSVSRVGOEHCLHPKLOSTKREIK 97
 Db 62 CAAQTEVIATLKND-----GHEVCLNPPAPLVQRIIVQ 91

RESULT 7

S215614
 macrophage inflammatory protein-2 - rat
 C:Species: Rattus sp. (rat)
 C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 20-Aug-1999
 C:Accession: I55614
 R:Feng, L.; Xia, Y.; Yoshimura, T.; Wilson, C.B.
 J. Clin. Invest. 95, 1009-1017, 1995
 A:Title: Modulation of neutrophil influx in glomerulonephritis in the rat with anti-macr
 A:Reference number: I55614; MUID:95189993
 A:Accession: I55614
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-100 <RES>
 A:Cross-references: GB:S77604; NID:9996406; PIDN:AA833749.1; PID:9996407
 C:Superfamily: beta-thromboglobulin

Query Match 21.1%; Score 124; DB 2; Length 100;
 Best local similarity 33.7%; Pred. No. 6.3e-06;

Matches 32; Conservative 16; Mismatches 37; Indels 10; Gaps 3;

OY 8 APPVSRMLAALALLLLALY---TARVDS--KCKCRKRPKIRYSDVKLEMKPKYPH 62
 Db 2 APPTRQLNNAVILVLLLLATNHHOGTGVVVAASELRQCILTLTPRVDFKNIQSLTVTPPGPH 61

OY 63 CEEKMWITTKSVSRVGOEHCLHPKLOSTKREIK 97
 Db 62 CAAQTEVIATLKND-----GHEVCLNPPAPLVQRIIVQ 91

RESULT 8

A28414
 melanoma growth-stimulatory activity precursor - human
 N:Alternate names: fibroblast-derived neutrophil-activating protein gamma; GRO-alpha.
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 20-Aug-1999
 C:Accession: S13669; A28414; S00983; B60401; S03976; A47626; B46519
 R:Baker, N.E.; Kucera, G.; Richmond, A.
 Nucleic Acids Res. 18, 6453, 1990
 A:Title: Nucleotide sequence of the human melanoma growth stimulatory activity (MGS)
 A:Reference number: S13669; MUID:91057157
 A:Accession: S13669
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-107 <BAR>
 A:Cross-references: EMBL:X54489; NID:934625; PIDN:CAA38361.1; PID:934626
 R:Antisowicz, A.; Bardwell, L.; Sager, R.
 Proc. Natl. Acad. Sci. U.S.A. 84, 7188-7192, 1987
 A:Title: Constitutive overexpression of a growth-regulated gene in transformed Chinese
 A:Reference number: A24184; MUID:88041072
 A:Accession: A28414
 A:Molecule type: mRNA
 A:Residues: 1-107 <ANT>
 A:Cross-references: GB:J03561; NID:9183622; PIDN:AAA35933.1; PID:9306806
 R:Richmond, A.; Balentien, E.; Thomas, H.G.; Flagg, G.; Barton, D.E.; Spiess, J.; Bo
 EMBO J. 7, 2025-2033, 1988
 A:Title: Molecular characterization and chromosomal mapping of melanoma growth stimu
 A:Reference number: S00983; MUID:88328991
 A:Accession: S00983
 A:Molecule type: mRNA
 A:Residues: 1-107 <RIC>
 A:Cross-references: EMBL:X12510; NID:934621; PIDN:CAA31027.1; PID:934622
 R:Schroeder, J.M.; Sticherling, M.; Henneicke, H.H.; Preissner, W.C.; Christophers, E
 J. Immunol. 144, 2223-2232, 1990
 A:Title: IL-1alpha or tumor necrosis factor-alpha stimulate release of three NAP-1/IL
 A:Reference number: A60401; MUID:90187866
 A:Accession: B60401
 A:Molecule type: protein
 A:Residues: 35-42, 'X', '44', 'X', '46-48 <SCH>
 A:Experimental source: dermal fibroblasts
 R:Golds, E.E.; Mason, P.; Nyirkos, P.
 Biochem. J. 259, 585-588, 1989
 A:Title: Inflammatory cytokines induce synthesis and secretion of gro protein and a n
 A:Reference number: S03975; MUID:89246368
 A:Accession: S03976
 A:Molecule type: protein
 A:Residues: 35-41, 'X', '43-49', 'X', '51-52', 'XX', '55-57 <GOL>
 R:Schroeder, J.M.; Peterson, N.L.M.; Christophers, E.
 J. Exp. Med. 171, 1091-1100, 1990
 A:Title: Lipopolysaccharide-stimulated human monocytes secrete, apart from neutrophil
 nity with melanoma growth stimulatory activity.
 A:Reference number: A47626; MUID:90217938
 A:Accession: A47626
 A:Molecule type: protein
 A:Residues: 35-63, 'X', '65 <SG2>
 A:Experimental source: LPS-stimulated monocytes
 R:Proost, P.; De Wolt-Peeters, C.; Conings, R.; Opdenakker, G.; Billiau, A.; Van Damm
 J. Immunol. 150, 1000-1010, 1993
 A:Title: Identification of a novel granulocyte chemotactic protein (GCP-2) from human
 A:Reference number: A46519; MUID:91139489
 A:Accession: B46519
 A:Molecule type: protein
 A:Residues: 35-62 <PRO>
 A:Experimental source: MG-63 osteosarcoma cells
 C:Genetics:
 A:Gene: GDB:GR01
 A:Cross-references: GDB:120181; OMIM:155730
 A:Map position: 4q21-4q21

RESULT 12
JN0572
neutrophil chemo-attractant Gro protein precursor - rat
N:Alternate names: CINC; cytokine-induced neutrophil chemottractant; interleukin-8-like
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000
C:Accession: JN0572; J01519; A34481; A48988; S51214
R:Konishi, K.; Takata, Y.; Yamamoto, M.; Yomogida, K.; Tsurufuji, S.; Fujii
Gene 126, 285-286, 1993
A:Title: Structure of the gene encoding rat neutrophil chemo-attractant Gro.
A:Reference number: JN0572; MUID:93246259
A:Accession: JN0572

A:Molecule type: DNA
A:Residues: 1-96 <KON>
A:Cross-references: DDBJ:D11445; NID:9391854; PIDN:BAA02009.1; PID:9220755
R:Huang, S.; Paulauskis, J.D.; Kobzik, L.
Biochem. Biophys. Res. Commun. 184, 922-929, 1992
A:Title: Rat KC cDNA cloning and mRNA expression in lung macrophages and fibroblasts.
A:Reference number: J01519; MUID:92246987
A:Accession: J01519

A:Molecule type: mRNA
A:Residues: 1-32, 'S', '34-96 <HUA>
A:Cross-references: GB:M6536
A:Experimental source: alveolar macrophage
A>Note: the authors translated the codon AGT for residue 33 as Cys, AAC for residue 46 as
R:Watanabe, K.; Konishi, K.; Fujioka, M.; Kinoshita, S.; Nakagawa, H.
J. Biol. Chem. 264, 19559-19563, 1989
A:Title: The neutrophil chemoattractant produced by the rat kidney epitheloid cell line
A:Reference number: A34481; MUID:90062049
A:Accession: A34481

A:Molecule type: protein
A:Residues: 25-96 <NAT>
R:Nakagawa, H.; Ikeue, A.; Hatakeyama, S.; Kato, H.; Gotoda, T.; Komorita, N.; Watanabe
Biochem. Pharmacol. 45, 1423-1430, 1993
A:Title: Production of an interleukin-8-like chemokine by cytokine-stimulated rat NRK-49
A:Reference number: A48988; MUID:9228656
A:Accession: A48988

A:Status: preliminary
A:Molecule type: protein
A:Residues: 25-57 <NAK>
A:Experimental source: kidney, NRK-49F fibroblasts
A:Note: sequence extracted from NCBI backbone (NCBI:P:129132)
A:Accession: B48988

A:Status: preliminary
A:Molecule type: protein
A:Residues: 25-57 <NA2>
A:Experimental source: kidney, NRK-49F fibroblasts
A:Note: sequence extracted from NCBI backbone (NCBI:P:129131)
R:Hanzawa, H.; Haruyama, H.; Watanabe, K.; Tsurufuji, S.
FEBS Lett. 354, 207-212, 1994
A:Title: The three dimensional structure of rat cytokine CINC/Gro in solution by homonud
A:Reference number: S51214; MUID:95046335
A:Contents: annotation; conformation by (1)H-NMR, residues 25-96
A:Accession: S51214

A:Molecule type: protein
A:Residues: 25-96 <HAN>
C:Comment: This protein has chemotactic activity for neutrophils and has melanoma growth
C:Genetics:
A:Gene: gro; KC
A:Intons: 24/1; 65/2; 92/2
C:Superfamily: beta-thromboglobulin
C:Keywords: cytokine; disulfide bond
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-96/Product: neutrophil chemo-attractant Gro protein #status experimental <CYT>

Query Match 16.5%; Score 97; DB 2; Length 96;
Best Local Similarity 27.8%; Pred. No. 0.004;
Matches 25; Conservative 20; Mismatches 29; Indels 16; Gaps 3;

OY 15 LAAALLLLLLAITYTAR-----VDGSKCKSGKPKIRYSDVKLEMKPKYPHCEK 67
DB 8 LTAALPVL-----TSRQATGAPVANELRCQGLQTVAGIHFKNIQSLKVPKPPHCTQTE 63

OY 68 VIITPKSVRYGOEHCLPKLOSTKRRIK 97
DB 64 VIATLKN-----GRDACLDPAPVQKIVQ 88

RESULT 13
A35766
platelet factor 4, interferon gamma-induced, precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 05-Oct-1990 #sequence_revision 05-Oct-1990 #text_change 20-Aug-1999
C:Accession: A35766
R:Farber, J.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 5238-5242, 1990
A:Title: A macrophage mRNA selectively induced by gamma-interferon encodes a member o
A:Reference number: A35766; MUID:90319087
A:Accession: A35766
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-126 <FAR>
A:Cross-references: GB:M34815; NID:q199692; PIDN:AAA39706.1; PID:q199693
C:Superfamily: beta-thromboglobulin

Query Match 16.1%; Score 94.5; DB 2; Length 126;
Best Local Similarity 25.5%; Pred. No. 0.0093;
Matches 26; Conservative 21; Mismatches 40; Indels 15; Gaps 4;

OY 16 LAAALLLLLLAITY-----TARVDGSKCK-SRKGPRIYSDVKLEMKPKYPHCEK 66
DB 1 MRSAYLEFLILIEQCGVGTIVRNARCSISTSGRTIHYKSLDKQFAPSPNCMT 60

OY 67 MVITPKSVRYGOEHCLPKLOSTKRRIK-WYNMNEKRR 107
DB 61 EITLTKN-----GDQTCIDPDSANVAKLKEKKEKINDK 97

RESULT 14
JN0470
interferon gamma-induced protein HUMIG - human
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 28-May-1999
C:Accession: JN0470
R:Farber, J.M.
Biochem. Biophys. Res. Commun. 192, 223-230, 1993
A:Title: Humig: a new human member of the chemokine family of cytokines.
A:Reference number: JN0470; MUID:93236577
A:Accession: JN0470
A:Molecule type: mRNA
A:Residues: 1-125 <FAR>
A:Cross-references: GB:X72755; GB:S60728; NID:g311375; PIDN:CAA51284.1; PID:g311376
C:Superfamily: beta-thromboglobulin
C:Keywords: cytokine

Query Match 14.9%; Score 87.5; DB 2; Length 125;
Best Local Similarity 29.5%; Pred. No. 0.05;
Matches 28; Conservative 14; Mismatches 46; Indels 7; Gaps 3;

OY 15 LAAALLLLLLAITYTARVDGSKCK-SRKGPRIYSDVKLEMKPKYPHCEK 73
DB 9 LAGTILLVILIGVGTIVRNARCSISTSGRTIHYKSLDKQFAPSPCEK 68

OY 74 SVSRFYGOEHCLPKLOSTKRRI-KWYNMNEKRR 107
DB 69 N-----GVQTCIDPDSADYKELIKKEKOVSO 98

RESULT 15
151886
macrophage inflammatory protein-2 - rat (fragment)
C:Species: Rattus sp. (rat)
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 16-Feb-1997

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 29, 2002, 16:03:34 ; Search time 11.67 Seconds
(without alignments)

348.740 Million cell updates/sec

Title: US-09-978-189-370

Perfect score: 587
Sequence: 1 MSLPFRAPVSMRLAAL.....TKRFIKWYNAMEKRYEE 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	527	89.8	99	S214_HUMAN	O95715 homo sapien
2	489	83.3	99	S214_MOUSE	O95715 mus musculi
3	143.5	24.4	100	M12B_RAT	O10747 rattus norv
4	138	23.5	100	M12P_MOUSE	P10889 mus musculi
5	131	22.3	101	GRO_CRIGR	P09340 cricetus
6	128.5	21.9	107	M12A_HUMAN	P19875 homo sapien
7	127.5	21.7	103	GRO_SHEEP	O46678 ovis aries
8	124	21.1	100	M12P_RAT	P30348 rattus norv
9	122.5	20.9	98	GRO_BOVIN	O46675 bos taurus
10	118.5	20.2	104	GRO_RABIT	P47854 oryctolagus
11	117.5	20.0	104	GRO_BOVIN	O46677 bos taurus
12	117.5	20.0	107	GRO_HUMAN	P09341 homo sapien
13	116.5	19.8	107	M12B_HUMAN	P19876 homo sapien
14	113.5	19.3	104	GRO_BOVIN	O46676 bos taurus
15	111	18.9	96	GRO_MOUSE	P12850 mus musculi
16	104.5	17.8	68	M12A_RAT	O10746 rattus norv
17	103	17.5	104	GRO_CAVPO	O55335 cavia porce
18	103	17.5	117	AMC2_PIG	P22952 sus scrofa
19	97	16.5	96	GRO_RAT	P14695 rattus norv
20	94.5	16.1	126	S203_MOUSE	P18340 mus musculi
21	90.5	15.4	71	GRO1_RABIT	P30782 oryctolagus
22	87.5	14.9	125	S206_HUMAN	O07325 homo sapien
23	87	14.8	114	S206_HUMAN	P80162 homo sapien
24	86	14.7	112	S206_BOVIN	P80231 bos taurus
25	84	14.3	94	S211_HUMAN	O14625 homo sapien
26	84	14.3	104	PLFV_HUMAN	P10720 homo sapien
27	83.5	14.2	101	IL8_CANFA	P41324 canis famill
28	82.5	14.1	103	IL8_PIG	P26894 sus scrofa
29	82.5	14.0	128	PF4L_HUMAN	P02775 homo sapien
30	82	14.0	94	SY26_HUMAN	O92558 homo sapien
31	82	14.0	130	S205_RAT	P97885 rattus norv
32	81	13.8	101	PLF4_HUMAN	P02776 homo sapien
33	80.5	13.7	98	S210_MOUSE	P17515 mus musculi

34	80.5	13.7	101	IL8_BOVIN	P79255 bos taurus
35	80.5	13.7	103	EMF1_CHICK	P08317 gallus gall.
36	80	13.6	119	PF4L_PIG	P43030 sus scrofa
37	79.5	13.5	98	S210_HUMAN	P02778 homo sapien
38	79.5	13.5	101	IL8_SHEEP	P36925 ovis aries
39	76.5	13.0	114	S205_HUMAN	P42830 homo sapien
40	76	12.9	132	S205_MOUSE	P50228 mus musculi
41	75.5	12.9	97	IL8_HORSE	O62812 equus caball
42	73	12.4	89	SY18_HUMAN	P55774 h small ind
43	73	12.4	105	PLF4_RAT	P06765 rattus norv
44	72.5	12.4	101	IL8_RABIT	P19874 oryctolagus
45	72	12.3	101	IL8_MACMU	P51495 macaca mula

ALIGNMENTS

RESULT	ID	STANDARD	PRT	99 AA
1	S214_HUMAN			
AC	O95715;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	SMALL INDUCIBLE CYTOKINE B14 PRECURSOR (CHEMOKINE BRK).			
GN	SCYB14 OR NJAC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Carnivora; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99160416; PubMed=10049774;			
RA	Hromas R., Broxmeyer H.E., Kim C., Nakshatri H., Christopherson K. II,			
RA	Azam M., Hou Y.-H.;			
RT	"Cloning of BRK, a novel divergent CXC chemokine preferentially			
RT	expressed in normal versus malignant cells.";			
RL	Biochem. Biophys. Res. Commun. 255:703-706(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Oral epithelium;			
RA	Frederick M.F., Henderson Y., Xu X., El-Naggar A.K., Wu H.,			
RA	Hudson J.M., Clayman G.L.;			
RL	Submitted (Apr-1999) to the EMBL/Genbank/DBJ databases.			
CC	- FUNCTION: NOT CHEMOTACTIVE FOR T-CELLS, B-CELLS, MONOCYTES,			
CC	NATURAL KILLER CELLS OR GRANULOCYTES. DOES NOT INHIBIT			
CC	PROLIFERATION OF MYELOID PROGENITORS IN COLONY FORMATION ASSAYS.			
CC	- TISSUE SPECIFICITY: EXPRESSED IN HEART, BRAIN, PLACENTA, LUNG,			
CC	LIVER, SKELETAL MUSCLE, KIDNEY, AND PANCREAS. HIGHLY EXPRESSED IN			
CC	NORMAL TISSUE WITHOUT INFLAMMATORY STIMULI AND INFREQUENTLY			
CC	EXPRESSED IN CANCER CELL LINES.			
CC	- SIMILARITY: BELONGS TO THE INTERFERON ALPHA FAMILY (SMALL CYTOKINE			
CC	C-X-C) (CHEMOKINE CXC).			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
CC	EMBL: AF079957; AAD03839.1; -			
CC	EMBL: AF144103; AAD38944.1; -			
CC	-----			
DR	InterPro: IPR001811; Chemokine_IL8.			
DR	InterPro: IPR001089; Small_cytokine_CXC.			
DR	PRINTS: PR00436; INTERLEUKIN8.			
DR	SMART: SM00199; SCY; 1.			
DR	PROSITE: PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.			
KW	Cytokine; Signal.			
FT	SIGNAL 1 22			POTENTIAL.
FT	CHAIN 23 99			SMALL INDUCIBLE CYTOKINE B14.

FT DISULFID 25 51 BY SIMILARITY.
 FT DISULFID 27 72 BY SIMILARITY.
 SQ SEQUENCE 99 AA: 11772 MW: 998802D8FC659C1D CRC64;

Query Match 89.8%; Score 527; DB 1; Length 99;
 Best Local Similarity 100.0%; Pred. No. 2,8e-49;
 Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 MRLAALLLLLLALYTRAVDGSCKCCKSGPKIRYSDVKLEMKPKYPHCEEKWITTT 72
 |||
 DB 1 MRLAALLLLLLALYTRAVDGSCKCCKSGPKIRYSDVKLEMKPKYPHCEEKWITTT 60

OY 73 KVSRYRGQEHCLHPKLOSTKRFIKWYNNANNEKRYEE 111
 |||
 DB 61 KVSRYRGQEHCLHPKLOSTKRFIKWYNNANNEKRYEE 99

RESULT 2
 S214_MOUSE STANDARD; PRT; 99 AA.

ID S214_MOUSE
 AC O9WU05;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE SMALL INDUCIBLE CYTOKINE B14 PRECURSOR (CHEMOKINE BRAK) (KIDNEY-
 EXPRESSED CHEMOKINE CXC).
 OS SCYB14 OR KEC.
 GN Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99160416; PubMed=10049774;
 RA Hromas R., Broxmeyer H.E., Kim C., Nakhatri H., Christopherson K. II,
 RA Azam M., Hou Y.-H.;
 RT "Cloning of BRAK, a novel divergent CXC chemokine preferentially
 RT expressed in normal versus malignant cells."
 RL Biochem. Biophys. Res. Commun. 255:703-706(1999).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=C3H;
 RA Wang L., Deng L., Raikwar N., Sahota A., Tischfield J.A.;
 RT "Identification of a kidney-expressed chemokine (KEC), a member of the
 RT CXC family, that is selectively elevated in apt knockout mice."
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 CC -I- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
 C-X-C) (CHEMOKINE CXC).

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DR EMBL: AF152377; AAD34157.1; -
 DR EMBL: AF192557; AF03753.1; -
 DR MGD: MGI:1888514; Scybl4.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR InterPro: IPR001089; Small_cytokine_CXC.
 DR PRINTS: PR00436; INTERLEUKIN8.
 DR SMART: SM00199; SCY; 1.

DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; FALSE_NEG.

FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 99 SMALL INDUCIBLE CYTOKINE B14.
 FT DISULFID 25 51 BY SIMILARITY.

FT DISULFID 27 72 BY SIMILARITY.
 FT CONFLICT 64 64 F -> S (IN REF. 2).
 FT SEQUENCE 99 AA: 11802 MW: 754B6CDA01CA25D CRC64;

Query Match 83.3%; Score 489; DB 1; Length 99;
 Best Local Similarity 91.9%; Pred. No. 3e-45;
 Matches 91; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 13 MRLAALLLLLLALYTRAVDGSCKCCKSGPKIRYSDVKLEMKPKYPHCEEKWITTT 72
 |||
 DB 1 MRLAALLLLLLALYTRAVDGSCKCCKSGPKIRYSDVKLEMKPKYPHCEEKWITTT 60

OY 73 KVSRYRGQEHCLHPKLOSTKRFIKWYNNANNEKRYEE 111
 |||
 DB 61 KVSRYRGQEHCLHPKLOSTKRFIKWYNNANNEKRYEE 99

RESULT 3
 M12B_RAT STANDARD; PRT; 100 AA.

ID M12B_RAT
 AC Q10747;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE MACROPHAGE INFLAMMATORY PROTEIN-2-BETA PRECURSOR (MIP2-BETA) (CINC-
 2-BETA).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;

RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 33-100.
 RC STRAIN=M12B;
 RX MEDLINE=94318061; PubMed=8043001;
 RA Nakagawa H., Komorita N., Shibata F., Ikeue A., Konishi K.,
 RA Fujioka M., Kato H.;
 RT "Identification of cytokine-induced neutrophil chemoattractants
 RT (CINC), rat GRO/CINC-2 alpha and CINC-2 beta, produced by granulation
 RT tissue in culture: purification, complete amino acid sequences and
 RT characterization."
 RL Biochem. J. 301:545-550(1994).
 RN [2]

RP SEQUENCE OF 33-52.
 RC STRAIN=M12B;
 RX MEDLINE=96183056; PubMed=8607872;
 RA Nakagawa H., Shiota S., Takano K., Shibata F., Kato H.;
 RT "Cytokine-induced neutrophil chemoattractant (CINC)-2 alpha, a novel
 RT member of rat GRO/CINCS, is a predominant chemokine produced by
 RT lipopolysaccharide-stimulated rat macrophages in culture."
 RL Biochem. Biophys. Res. Commun. 220:945-948(1996).
 CC -I- FUNCTION: MAY PLAY A ROLE IN INFLAMMATION AND EXERT ITS EFFECTS
 CC ON ENDOTHELIAL CELLS IN AN AUTOCRINE FASHION.
 CC -I- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
 C-X-C) (CHEMOKINE CXC).

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DR EMBL: D21095; BAA04657.1; -
 DR HSP: P10889; M12.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR InterPro: IPR001089; Small_cytokine_CXC.
 DR Pfam: PF00048; IL8; 1.
 DR PRINTS: PR00436; INTERLEUKIN8.
 DR PRINTS: PR00437; SMALLCYTCKXC.
 DR SMART: SM00199; SCY; 1.

DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
 DR Cytokine; Chemotaxis; Inflammatory response; Signal.

FT SIGNAL 1 32
 FT CHAIN 33 100 MACROPHAGE INFLAMMATORY PROTEIN-

FT DISULFID 37 63 2-BETA.
 FT DISULFID 39 79 BY SIMILARITY.
 SO SEQUENCE 100 AA: 10989 MW: EB53ECFE30909D2 CRC64;

Query Match 24.4%; Score 143.5; DB 1; Length 100;
 Best Local Similarity 35.1%; Pred. No. 1.4e-08;
 Matches 34; Conservative 19; Mismatches 31; Indels 13; Gaps 3;

QY 8 APPVSRLLAALLLLALLALYARVDG-----KCKSRKSPKIRYSYVKKLEKPKY 60
 DB 2 APP-TRRLNALLLLALLMATSHOPSQTVVARELRQCKLTLPVDFENIQSLVTPPG 60
 QY 61 PCEEKVITTKRSYRSGEHLHPKLOSTKRFK 97
 DB 61 PCHQTEVATLKD-----GQVCLNPQAPRLQKIIQ 92

RESULT 4

MIP2_MOUSE STANDARD; PRT; 100 AA.

AC P10889;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE MACROPHAGE INFLAMMATORY PROTEIN 2 PRECURSOR (MIP2).
 GN SCYB2 OR MIP2 OR MIP-2.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90354792; PubMed=2201751;
 RA Tekamp-Olson P., Gallegos C., Bauer D., McClain J., Sherry B.,
 RA Febre M., van Deventer S., Cerami A.;
 RT Cloning and characterization of cDNAs for murine macrophage
 RT inflammatory protein 2 and its human homologues.";
 RL J. Exp. Med. 172:911-919(1990).
 RN [2]

RP SEQUENCE OF 28-59.
 RX MEDLINE=89098980; PubMed=2643119;
 RA Wolpe S.D., Sherry B., Juers D., Davatelis G., Yurt R.W., Cerami A.;
 RT Identification and characterization of macrophage inflammatory
 RT protein 2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:612-616(1989).
 RN [3]

RP STRUCTURE BY NMR.
 RX MEDLINE=98285558; PubMed=9622482;
 RA Shao W., Jerva L.F., West J., Lolits E., Schweitzer B.I.;
 RT "solution structure of murine macrophage inflammatory protein-2.";
 RL Biochemistry 37:8303-8313(1998).
 CC -1- FUNCTION: CHEMOTACTIC FOR HUMAN POLYMORPHONUCLEAR LEUKOCYTES BUT
 CC DOES NOT INDUCE CHEMOKINESIS OR AN OXIDATIVE BURST.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
 CC C-X-C) (CHEMOKINE CXCL).

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DR EMBL: X53798; CA37807.1; -
 DR PIR: JH0200; JH0200.
 DR PDB: 1MI2; 29-APR-98.
 DR MGD: MGI:1340094; Scyb2.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR InterPro: IPR001089; Small_cytokine_CXC.

DR Pfam: PF00048; IL8; 1.
 DR PRINTS: PRO0436; INTERLEUKIN8.
 DR PRINTS: PRO0437; SMALLCYTCKXC.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.

KW Cytokine; Chemotaxis; Inflammatory response; Signal; 3D-structure.
 FT SIGNAL 1 27
 FT CHAIN 28 100 MACROPHAGE INFLAMMATORY PROTEIN 2.
 FT DISULFID 36 62
 FT DISULFID 38 78
 SO SEQUENCE 100 AA: 10621 MW: B9EFOA3218E92B5 CRC64;

Query Match 23.5%; Score 138; DB 1; Length 100;
 Best Local Similarity 33.3%; Pred. No. 5.6e-08;
 Matches 32; Conservative 21; Mismatches 31; Indels 12; Gaps 3;

QY 8 APPVSRLLAALLLLALLALYARVDG-----KCKSRKSPKIRYSYVKKLEKPKY 61
 DB 2 APP-TRRLNALLLLALLMATSHOPSQTVVARELRQCKLTLPVDFENIQSLVTPPG 60
 QY 62 HCEEKVITTKRSYRSGEHLHPKLOSTKRFK 97
 DB 61 HCAQTEVATLKG-----GQVCLNPQAPRLQKIIQ 91

RESULT 5

GRO_CRIGR STANDARD; PRT; 101 AA.

AC P09340;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE GROWTH REGULATED PROTEIN PRECURSOR.
 GN SCYB1 OR GRO.
 OS Cricetulus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetulus.
 OX NCBI_TaxID=10029;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=88041072; PubMed=2890161;
 RA Anisowicz A., Bartwell U., Sager R.;
 RT "Constitutive overexpression of a growth-regulated gene in
 RT transformed Chinese hamster and human cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:7188-7192(1987).
 CC -1- FUNCTION: HAS CHEMOTACTIC ACTIVITY FOR NEUTROPHILS.

CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
 CC C-X-C) (CHEMOKINE CXCL).

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DR EMBL: J03560; AAA36985.1; -
 DR PIR: B28414; B28414.
 DR HSSP: P10889; 1MI2.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR InterPro: IPR001089; Small_cytokine_CXC.
 DR Pfam: PF00048; IL8; 1.
 DR PRINTS: PRO0436; INTERLEUKIN8.
 DR PRINTS: PRO0437; SMALLCYTCKXC.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
 KW Cytokine; Growth factor; Inflammatory response; Signal.
 FT SIGNAL 1 28
 FT CHAIN 29 101 POTENTIAL.
 FT DISULFID 37 63 GROWTH REGULATED PROTEIN.
 BY SIMILARITY.

FT	DISULFID	39	79	BY SIMILARITY.
SQ	SEQUENCE	101 AA;	10893 MW;	666FB7E9CC512019 CRC64;

Query Match	22.3%;	Score 131;	DB 1;	Length 101;
Best Local Similarity	31.68;	Pred. No. 3.1e-07;		
Matches	30;	Conservative	21;	Mismatches 32;
				Indels 12;
				Gaps 2

Qy 10 PVSARLLAAALLLLLLLALTYARV-----DGSKCKCSRKGPRIYSDVKLLKMPKYPH 62

Db 3 PATSSLLRAPLLLLLLIATSRKATGAPVANELRCQCLQTMGVHLKNIQSLKATPPPGPH 62

```

QY 63 CEKMWIITTSVSRKRGQEHCHLPKLOSTKPRIK 97
      | : ||| | : ||| ||| : : :
Db 63 CTQTEVIATLTKN-----GQEACLINPEAPMQRIVQ 92

```

RESULT	6
MI2A_HUMAN	
ID	MI2A_HUMAN
STANDARD;	
PRT;	107 AA

DT	01-FEB-1991 (Rel. 17, Created)
DT	01-FEB-1991 (Rel. 17, Last sequence update)
DT	20-AUG-2001 (Rel. 40, Last annotation update)

DE MACROPHAGE INFLAMMATORY PROTEIN-2-ALPHA PRECURSOR (MIP2-ALPHA) (GROWTH
DE REGULATED PROTEIN BETA) (GRO-BETA).
GN GRO2 OR GROB OR MIP2A.

05 Homo sapiens (Human).
06
07 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
08 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
09

OA	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
BC	MTCNN-Histidine }-meth-

RA Tekamp-Olson P., Gallegos C., Bauer D., McClain J., Sherry B.,
Fabre M., van Doornout S., Corradi A., et al. (2002) CD44 is
MEDLINE=90354792; PubMed=2201751;
RX 113307=histiocytic lymphoma;
AC

RT "Cloning and characterization of cDNAs for murine macrophage inflammatory protein 2 and its human homologues.", *J. Exp. Med.* 172:911-919 (1990)

SEQUENCE FROM N.A.
MEDLINE=90377259. PubMed=207821

RT monocytes: expression in leukocytes and wound tissue". RT

RL Mol. Cell. Biol. 10:5596-5599 (1990).
RN [3]
RP SEQUENCE FROM N.A.

RX MEDLINE=91017578; PubMed=2217207;
RA Haskell S., Peace A., Morris J., Sporn S.A., Anisowicz A., Lee S.W.
RA Smith T., Martin G., Ralph P., Sager R.;

RT "Identification of three related human G90 genes encoding cytokine
RT functions.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:7732-7736(1990).

RN [4]
RP SEQUENCE OF 35-107 FROM N.A.
RA Jang J.S., Kim B.E.;

Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases
[5]
STRUCTURE BY NMR OF 39-107.

RX MEDLINE=20069929; Pubmed=10600366;
 RA Qian Y.Q., Johanson K.O., McDevitt P.;
 RT "Nuclear magnetic resonance solution structure of truncated human

RT GRObeta [5-73] and its structural
RT family members GROalpha and IL-8.
RL J. Mol. Biol. 294:1065-1072(1999).

CC - FUNCTION: PRODUCED BY ACTIVATED MONOCYTES AND NEUTROPHILS AND
CC EXPRESSED AT SITES OF INFLAMMATION.
CC - SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC FAMILY).

CC C-X-C) (CHEMOKINE CXC).
CC
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DR EMBL; M36820; AAA63183.1; -.
DR EMBL; M57731; AAA63182.1; -.
DR EMBL; AF043340; AAC03540.1; -

DR	PDB; 1QNK; 04-FEB-00.
DR	MIM; 139110; -.
DR	InterPro; IPR001811; Chemokine

DR PRINTS; PR00436; INTERLEUKIN8.
DR PRINTS; PR00437; SMALLCYTKCXC.
DR SMART; SM00199; SCY; 1.

KW	Cytokine; Chemotaxis; Inflammatory response; Signal; 3D-structure
FT	SIGNAL 1 34
FT	CHAIN 35 107 MACROPHAGE INFLAMMATORY PROTEIN-

	2-ALPHA.
FT	69
FT	43
FT	45
DISULFID	85

SQ SEQUENCE 107 AA; 11389 MW; 740F277E928571BA CRC64;

Query Match	21.9%	Score 128.5	DB 1	Length 107;
Best Local Similarity	33.3%	Pred. No. 6.1e-07;		
Matches 32; Conservative	18;	Mismatches 35;	Indels 11;	Gaps 2

QY 8 APVSMRLIAALLLLLLALYTARYDGS-----KCKCSRKGPIRYSVDYKLEMPKYP 61

DB 8 AAPSNPRLRLVALLLLLVASRRACAPLATELRCGL
QY 62 HCEEKVLIITKTSVSRVRCQEHCLHPKIQSTKRFIK 97

Db 68 HCAQTETVIATLKN---GQKACLNPPASPMVKKIIE 98

TD	CBO	CUMED	STANDARD	PRE	103
GRO_SHEEP					
RESULT					7

ID	GRV_SHEEP	STANDARD;	FRI;	103 AA.
AC	046678;			
DT	30-MAY-2000	(Rel. 39, Created)		
DT	30-MAY-2000	(Rel. 39, Last sequence updated)		

SCV41 OR GRO
GROWTH REGULATED PROTEIN PRECURSOR.
DE
DT 20-AUG-2001 (Rel. 40, last annotation update)
CA 20-APR-2000 (rel. 37, last sequence update)
GN

05 Ovis aries (Sheep).
06 Cervidae (Antelope).
0C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
0C Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Decora; Bovidae

OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
[1]

RP SEQUENCE FROM N.A.
RA Yoshimura T., Modi W.S.;
RT "Isolation of novel GRO genes, and a phylogenetic analysis of the CXCR4

chemokine subfamily in mammals.";
Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases
-!- FUNCTION: HAS CHEMOTACTIC ACTIVITY FOR NEUTROPHILS.

CC -I- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXC).
CC -----
CC

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DR 15-DEC-1998 (Rel. 37, Created)
DR 15-DEC-1998 (Rel. 37, Last sequence update)
DR 15-DEC-1998 (Rel. 37, Last annotation update)
DE GROWTH REGULATED PROTEIN HOMOLOG GAMMA PRECURSOR (GRO-GAMMA).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Yoshimura T., Modi W.S.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXC).
CC -----
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CC -----
CC EMBL: U95811; AAB93927.1; -
DR InterPro: IPR001811; Chemokine_IL8.
DR InterPro: IPR001089; Small_cytokine_CXC.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00437; SMALLCYTCKXC.
DR SMART: SM00199; SCT; 1.
DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
DR Cytokine; Growth factor; Inflammatory response; signal.
KW Cytokine; Growth factor; Inflammatory response; signal.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 98 GROWTH REGULATED PROTEIN HOMOLOG GAMMA.
FT DISULFID 39 65 BY SIMILARITY.
FT DISULFID 41 81 BY SIMILARITY.
SQ SEQUENCE 98 AA; 10393 MW; 942CD6897C21DE9 CRC64;

Query Match 20.9%; Score 122.5; DB 1; Length 98;
Best Local Similarity 34.0%; Pred. No. 2,4e-06;
Matches 33; Conservative 16; Mismatches 35; Indels 13; Gaps 3;

OY 8 APPVSM-RLAALLLLLLALYARVDS-----KCGSRGKGPKIRYSVYKLEMPK 59
Db 2 APAASAPRLRLAALLLLLLAAGRAAGAPVVELRCQCLDTLOGIHLKNISQKVTP 61
OY 60 YPCEKMWITTSVSRRCQEHRLPKLSTKRFI 96
Db 62 GPHCDQTEVIADTKT-----GQEVCLNAPAAWVKTI 93

RESULT 10
GRO2_RABIT
ID GRO2_RABIT STANDARD; PRT; 104 AA.
AC P47854;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE GROWTH REGULATED PROTEIN HOMOLOG PRECURSOR (GRO HOMOLOG).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Schwartz D., Chaverri-Alameda L., Berliner J., Kirchgessner T.,
RA Quintomoro D., Fang J., Tekamp-Olson P., Luisi J., Fogelman A.,
RA Terrio M.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PLAYS A ROLE IN MONOCYTE ADHESION TO THE ENDOTHELIUM.
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXC).
```

[illegible]

Best Local Similarity 32.3%; Pred. No. 8.9e-06;
Matches 31; Conservative 17; Mismatches 37; Indels 11; Gaps 2;

QY 8 APPVSMRLAALLLLALTYARVDS-----KCKSRKGPRTIRSDVKKLEMKPKYP 61
| : | | | | | | | | : : : : :
Db 8 AAPSNRLRLVALLLLVAAAGRAAGAVATLRCQCLQTLQGIHLNKIQSVNRSPGP 67
| : | | | | | | | | : : : : :
QY 62 HCEEMVITTTKSVSRVGRGECPLPKLOSTKRFK 97
| : | | | | | | | | : : : : :
Db 68 HCAQTEVIATLKN-----GKKACLNPAFSPVVKITE 98

RESULT 13

M12B_HUMAN

STANDARD;

PRT;

107 AA.

AC P19876; 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE MACROPHAGE INFLAMMATORY PROTEIN-2-BETA PRECURSOR (MIP2-BETA) (GROWTH
REGULATED PROTEIN GAMMA) (GRO-GAMMA).
GN GRO3 OR GROG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Histiocytic Lymphoma;

RX MEDLINE=90354792; PubMed=2201751;

RA Tekamp-Olson P., Gallegos C., Bauer D., McClain J., Sherry B.,

FA Fabre M., Van Deventer S., Cerami A.;

RT "Cloning and characterization of cDNAs for murine macrophage

RL inflammatory protein 2 and its human homologues.";

RN J. Exp. Med. 172:911-919(1990).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=91017578; PubMed=2217207;

RA Haskill S., Pearce A., Morris J., Sporn S.A., Anisowicz A., Lee S.W.,

RT Smith T., Martin G., Ralph P., Sager R.;

RT "Identification of three related human GRO genes encoding cytokine

RT functions.";

RL Proc. Natl. Acad. Sci. U.S.A. 87:7732-7736(1990).

CC -1- FUNCTION: MAY PLAY A ROLE IN INFLAMMATION AND EXERT ITS EFFECTS

CC ON ENDOMETRIAL CELLS IN AN AUTOCRINE FASHION

CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE

CC C-X-C) (CHEMOKINE CXCL).

CC -----

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CC -----

DR EMBL: X53800; CAA37809.1; -

DR EMBL: M36821; AAA63184.1; -

DR PIR: B38290; B38290.

DR PIR: JH0282; JH0282.

DR HSSP: P09341; IMGS.

DR MIM: 139111; -

DR InterPro: IPR001811; Chemokine_IL8.

DR InterPro: IPR001089; Small_cytokine_CXC.

DR Pfam: PF00048; IL8; 1.

DR PRINTS: PR00436; INTERLEUKIN8.

DR PRINTS: PR00437; SMALLCYTCKXC.

DR SMART: SM00199; SCY; 1.

DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.

DR CYTOKINE: Chemokines; Inflammatory response; Signal.

KW SIGNAL

FT CHAIN

FT 35 107

FT MACROPHAGE INFLAMMATORY PROTEIN-

FT 2-BETA.

FT DISULFID 43 69 BY SIMILARITY.
FT DISULFID 45 85 BY SIMILARITY.
FT CONFLICT 27 28 AA -> C (IN REF. 2).
SQ SEQUENCE 107 AA; 11342 MW; 97A69946B7F1F070 CRC64;

Query Match 19.8%; Score 116.5; DB 1; Length 107;
Best Local Similarity 30.2%; Pred. No. 1.1e-05;
Matches 29; Conservative 20; Mismatches 36; Indels 11; Gaps 2;

QY 8 APPVSMRLAALLLLALTYARVDS-----KCKSRKGPRTIRSDVKKLEMKPKYP 61
| : | | | | | | | | : : : : :
Db 8 AAPSNRLRLVALLLLVAAAGRAAGAVATLRCQCLQTLQGIHLNKIQSVNRSPGP 67
| : | | | | | | | | : : : : :
QY 62 HCEEMVITTTKSVSRVGRGECPLPKLOSTKRFK 97
| : | | | | | | | | : : : : :
Db 68 HCAQTEVIATLKN-----GKKACLNPAFSPVVKITE 98

RESULT 14

GROA_BOVIN

STANDARD;

PRT;

104 AA.

AC O46676; 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GROWTH REGULATED PROTEIN HOMOLOGY ALPHA PRECURSOR (GRO-ALPHA).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;

RN [1]

RP SEQUENCE FROM N.A.

RA Yoshimura T., Modi W.S.;

RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE

CC C-X-C) (CHEMOKINE CXCL).

CC -----

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CC -----

DR EMBL: U95812; AAB93928.1; -

DR InterPro: IPR001811; Chemokine_IL8.

DR InterPro: IPR001089; Small_cytokine_CXC.

DR Pfam: PF00048; IL8; 1.

DR PRINTS: PR00436; INTERLEUKIN8.

DR PRINTS: PR00437; SMALLCYTCKXC.

DR SMART: SM00199; SCY; 1.

DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.

KW Cytokine; Growth factor; Inflammatory response; Signal.

FT SIGNAL

FT CHAIN

FT 31 104

FT DISULFID 40 66

FT DISULFID 42 82

SQ SEQUENCE 104 AA; 10984 MW; 1002CAC064DB1F76 CRC64;

Query Match 19.3%; Score 113.5; DB 1; Length 104;
Best Local Similarity 30.5%; Pred. No. 2.3e-05;
Matches 29; Conservative 18; Mismatches 37; Indels 11; Gaps 2;

QY 8 APPVSMRLAALLLLALTYARVDS-----KCKSRKGPRTIRSDVKKLEMKPKYP 61
| : | | | | | | | | : : : : :
Db 5 ATPAARLRLAAMFLLLVAAAGRAAGAVATLRCQCLQTLQGIHLNKIQSVKVTTPGP 64
| : | | | | | | | | : : : : :
QY 62 HCEEMVITTTKSVSRVGRGECPLPKLOSTKRFK 96
| : | | | | | | | | : : : : :
| : | | | | | | | | : : : : :

Db 65 HCDTEVYASLKT-----GGEVCLNPTAPVKKII 94

RESULT 15

GRO_MOUSE STANDARD: PRT: 96 AA.

ID GRO_MOUSE P12850:

AC 01-OCT-1989 (Rel. 12, Created)

DT 01-OCT-1989 (Rel. 12, last sequence update)

DT 20-AUG-2001 (Rel. 40, last annotation update)

DE GROWTH REGULATED PROTEIN PRECURSOR (PLATELET-DERIVED GROWTH FACTOR-INDUCIBLE PROTEIN KC) (SECRETORY PROTEIN N51).

GN SCYB1 OR GRO1 OR GRO OR MGSA.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

11

RP SEQUENCE FROM N.A.

RX MEDLINE=89139485; PubMed=2917992;

RA Okendo P., Alberta J., Wen D., Graycar J.L., Derynck R., Stiles C.D.;

RT "The platelet-derived growth factor-inducible KC gene encodes a secretory protein related to platelet alpha-granule proteins.";

RL J. Biol. Chem. 264:4133-4137(1989).

12

RP SEQUENCE FROM N.A.

RX MEDLINE=89078502; PubMed=2909392;

RA Ryseck R.P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;

RT "Cloning and sequence of a secretory protein induced by growth factors in mouse fibroblasts.";

RL Exp. Cell Res. 180:266-275(1989).

13

RP SEQUENCE FROM N.A.

RX STRAIN=129/SV;

RA Bozic C.R., Kolakowski L.F. Jr., von Uexkull C., Garcia-Rodriguez M., Conklyn M.J., Breslow R., Showell H.J., Gerard N.P., Gerard C.;

RT Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.

14

RP SEQUENCE OF 1-10 FROM N.A.

RX TISSUE=Liver;

RA MEDLINE=96016008; PubMed=7561058;

RT Ohmori Y., Fukumoto S., Hamilton T.A.;

RT "Two structurally distinct kappa B sequence motifs cooperatively control LPS-induced KC gene transcription in mouse macrophages.";

RL J. Immunol. 155:3593-3600(1995).

15

RP FUNCTION: HAS CHEMOTACTIC ACTIVITY FOR NEUTROPHILS. CONTRIBUTES TO NEUTROPHIL ACTIVATION DURING INFLAMMATION (BY SIMILARITY).

16

RP INDUCTION: BY PLATELET-DERIVED GROWTH FACTOR. IN LUNG, BY LIPOPOLYSACCHARIDE OR INFLAMMATION (BY SIMILARITY).

17

RP SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE C-X-C) (CHEMOKINE CXK).

18

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19

EMBL: J04596; AAA0131.1;

EMBL: U20634; AAB03376.1;

EMBL: U20527; AAB03376.1; JOINED.

EMBL: S79767; -; NOT_ANNOTATED_CDS.

PIR: A32954; A32954.

PIR: JH0081; JH0081.

HSSP: P09341; IMSH.

MGD: MGT:108068; Grol.

InterPro: IPR001811; Chemokine_IL8.

InterPro: IPR001089; Small_cytokine_CXC.

Pfam: PF00048; IL8; 1.

PRINTS: PR00436; INTERLEUKIN8.

PRINTS: PR00437; SMALLCYTKXC.

DR SMART; SMO0199; SCY, 1.

DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.

KW Cytokine; Growth factor; Inflammatory response; Signal.

FT SIGNAL 1 24 PROBABLE.

FT CHAIN 25 96 GROWTH REGULATED PROTEIN.

FT DISULFID 33 59 BY SIMILARITY.

FT DISULFID 35 75 BY SIMILARITY.

SQ SEQUENCE 96 AA; 10254 MW; 4A52B5E5C38BA5C2 CRC64;

Query Match 18.9%; Score 111; DB 1; Length 96;

Best Local Similarity 30.8%; Pred. No. 3.9e-05;

Matches 28; Conservative 18; Mismatches 37; Indels 8; Gaps 2;

Qy 10 PYSMRLAALLLL---LALYARVDSKSKSRKGRIRSDVKLEMPKYPHCEK 66

Db 3 PATSLICALLLLTSTRATATCAPIANELRCOCLOTMAGIHKLNIOSIKVLPSPGHCTOT 62

Qy 67 MWIITTSVSRYSRGOEHLHPKLOSTKREK 97

Db 63 EVIATLKN-----GREACLDPEAPLVOKIVQ 88

Search completed: January 29, 2002, 16:05:34

Job time: 120 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 29, 2002, 16:03:34 ; Search time 22.64 Seconds

(without alignments)
717.148 Million cell updates/sec

Title: US-09-978-189-370

Perfect score: 587
Sequence: 1 MSLLPRRAPVPSMRLLAAL.....TKRKIKYNAWNEKRRVYEE 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 segs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP_invertebrate:*
6: SP_mammal:*
7: SP_mhc:*
8: SP-organelle:*
9: SP-Phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	587	100.0	111	4 Q9BTR1	Q9BTR1 homo sapien
2	582	99.1	111	4 Q9NS21	Q9NS21 homo sapien
3	506	86.2	99	11 Q9JHH7	Q9JHH7 mus musculu
4	371	57.1	100	13 Q9DFG4	Q9DFG4 brachydanio
5	322.5	54.9	98	13 Q9DGA8	Q9DGA8 gallus gall
6	143.5	24.4	101	11 Q9EP62	Q9EP62 rattus norv
7	128.5	21.9	98	6 Q28724	Q28724 oryctolagus
8	97.5	16.6	97	13 Q98TQ2	Q98TQ2 oncorhynch
9	93.5	15.9	126	11 Q9JUC6	Q9JUC6 mus musculu
10	89	15.2	113	11 Q9E015	Q9E015 mus musculu
11	87.5	14.9	111	11 Q9JME0	Q9JME0 rattus norv
12	86.5	14.7	104	13 Q73912	Q73912 gallus gall
13	86	14.7	93	13 Q9PTR8	Q9PTR8 brachydanio
14	83.5	14.2	101	6 Q9XSK5	Q9XSK5 felis silve
15	83.5	14.2	117	12 Q68398	Q68398 human cytom
16	76.5	13.0	59	6 Q62764	Q62764 equus cabal
17	76	12.9	98	11 Q9ERB1	Q9ERB1 mesocricetu
18	76	12.9	677	5 Q18209	Q18209 caenorhabdi
19	74.5	12.7	356	11 Q08889	Q08889 cricetus

20	74	12.6	394	5 Q44635	Q44635 caenorhabdi
21	72.5	12.4	131	13 Q9PY19	Q9PY19 harpadori
22	72.5	12.4	356	11 Q88464	Q88464 mus musculu
23	72.5	12.4	356	11 Q9JLK2	Q9JLK2 mus musculu
24	71.5	12.2	102	4 Q9C077	Q9C077 homo sapien
25	71.5	12.2	1417	5 Q9VSE1	Q9VSE1 drosophila
26	71	12.1	475	12 Q9QDL4	Q9QDL4 pleione vir
27	71	12.1	1270	5 Q23658	Q23658 caenorhabdi
28	70.5	12.0	356	4 Q75036	Q75036 homo sapien
29	70	11.9	101	13 Q93442	Q93442 lampetra fl
30	69	11.8	599	4 Q9P0M8	Q9P0M8 homo sapien
31	68.5	11.7	97	11 Q9Z318	Q9Z318 cavia porce
32	68	11.6	149	5 Q22745	Q22745 caenorhabdi
33	68	11.6	204	10 Q9M5N2	Q9M5N2 aegilops ve
34	68	11.6	581	1 Q9H0Y4	Q9H0Y4 halobacteri
35	68	11.6	751	11 P70535	P70535 rattus norv
36	67	11.4	647	4 Q94815	Q94815 homo sapien
37	67	11.4	648	4 Q9UP38	Q9UP38 homo sapien
38	66.5	11.3	86	11 Q9QX28	Q9QX28 mus musculu
39	66.5	11.3	272	5 Q9VEM6	Q9VEM6 drosophila
40	66.5	11.3	346	2 P70801	P70801 anabaena va
41	66.5	11.3	397	2 Q66569	Q66569 aquifex aeo
42	66.5	11.3	1632	5 Q9NDH2	Q9NDH2 caenorhabdi
43	66.5	11.3	3228	5 Q93593	Q93593 caenorhabdi
44	66	11.2	346	4 Q14877	Q14877 homo sapien
45	66	11.2	6815	5 Q91704	Q91704 drosophila

ALIGNMENTS

RESULT	ID	Q9BTR1	PRELIMINARY:	PRT:	111 AA.
Q9BTR1	Q9BTR1	Q9BTR1	Q9BTR1	Q9BTR1	Q9BTR1
DT	01-JUN-2001	(TREMBLrel. 17, Created)			
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)			
DE	01-JUN-2001	(TREMBLrel. 17, Last annotation update)			
DE	SMALL INDICIBLE CYTOKINE SUBFAMILY B (CYS-X-CYS), MEMBER 14 (BRK).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=PANCREATIC ADENOCARCINOMA;				
RA	Straussberg R.;				
RL	Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.				
DR	EMBL, BC003513; AA03513.1;				
DR	SEQUENCE 111 AA; 13077 MW; C9A18B2A/8CACE74 CRC64;				
Query Match	Best Local Similarity	100.0%; Score 587; DB 4; Length 111;			
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	1	MSLLPRRAPVPSMRLLAALLLLALTYARVDSKCKSKRGPRIRYSDVKLEMPKY 60			
DB	1	MSLLPRRAPVPSMRLLAALLLLALTYARVDSKCKSKRGPRIRYSDVKLEMPKY 60			
QY	61	PRCEKMWIITTKSVSRKRGDCHLPKLOSTKRIKYNWNEKRRVYEE 111			
DB	61	PRCEKMWIITTKSVSRKRGDCHLPKLOSTKRIKYNWNEKRRVYEE 111			
DB	61	PRCEKMWIITTKSVSRKRGDCHLPKLOSTKRIKYNWNEKRRVYEE 111			
RESULT	2	PRELIMINARY:	PRT:	111 AA.	
AC	Q9NS21	Q9NS21	Q9NS21	Q9NS21	Q9NS21
DT	01-OCT-2000	(TREMBLrel. 15, Created)			
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)			
DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)			
DE	CHEMOKINE MIP-2 GAMMA.				

GN MIP-2 GAMMA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
R Zhang W., Man T., Yuan Z., Cao X.;
RT "A novel chemokine gene, MIP-2 gamma,"
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF106911; AAF78449.1; -
DR InterPro; IPR001811; Chemokine_IL8.
DR SMART; SM00199; SCY; 1.
SQ SEQUENCE 111 AA; 13126 MW; C9A18B3178CACE74 CRC64;

Query Match 99.1%; Score 582; DB 4; Length 111;
Best Local Similarity 99.1%; Pred. No. 2.4e-57;
Matches 110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSLLPRAPVSMRLAALLLLLTARVDGSKCKSRGPKIRYSDVKLEKPKY 60
D 1 MSLLPRAPVSMRLAALLLLLTARVDGSKCKSRGPKIRYSDVKLEKPKY 60
Db 1 MSLLPRAPVSMRLAALLLLLTARVDGSKCKSRGPKIRYSDVKLEKPKY 60

QY 61 PCEEEKVITTTKSVSRGQEHLPKLOSTKRFIKYNNANNEKRYVEE 111
D 61 PCEEEKVITTTKSVSRGQEHLPKLOSTKRFIKYNNANNEKRYVEE 111
Db 61 PCEEEKVITTTKSVSRGQEHLPKLOSTKRFIKYNNANNEKRYVEE 111

RESULT 3
Q9JHH7 PRELIMINARY; PRT; 99 AA.
AC Q9JHH7;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 17, Last sequence update)
DE B CELL AND MONOCYTE-ACTIVATING CHEMOKINE PRECURSOR (BRAIN CDNA, CLONE NMBC-6413), SIMILAR TO MUS MUSCULUS KIDNEY-EXPRESSED CHEMOKINE CXK (KEC) mRNA (KRC) (1200006123RIK PROTEIN).
GN SCYB14 OR BMAC OR 1200006123RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CBYJ;
RA Sleeman M.A., Fraser J.K., Murison J.G., Kelly S.L., Prestidge R., Watson J.D., Kumble K.D.;
RT "A cell and monocyte-activating chemokine (BMAC), a novel non-EHR alpha chemokine,"
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL;
RA Osada N., Kusuda J., Tanuma R., Ito A., Hirata M., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from mouse brain cDNA library made by oligo-capping method,"
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC HEAD, AND LUNG;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Konno S., Yamanaoka I., Saito T., Okazaki Y., Gojofori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Caslavac T., Fleischmann W., Gaasterland T., Gissi C., King B., Kociani H., Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J., Schmitt L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilmink L., Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S., Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection,"
RL Nature 409:685-690(2001).
DR EMBL; AF144754; AAF6694.1; -
DR EMBL; AB041614; BAA95097.1; -
DR EMBL; AK014351; BAB29292.1; -
DR EMBL; AK004615; BAB23411.1; -
DR MGD; MGI:1888514; Scybl4.
DR MGD; MGI:1915056; 1200006123RIK.
DR InterPro; IPR001811; Chemokine_IL8.
DR SMART; SM00199; SCY; 1.
KM Signal.
FT SIGNAL.
FT CHAIN 1 23 POTENTIAL.
FT 24 99 B CELL AND MONOCYTE-ACTIVATING
FT CHEMOKINE.
SQ SEQUENCE 99 AA; 11716 MW; 97352E91FF7F46D6 CRC64;

Query Match 86.2%; Score 506; DB 11; Length 99;
Best Local Similarity 94.9%; Pred. No. 6.3e-49;
Matches 94; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 13 MRLAALLLLLTARVDGSKCKSRGPKIRYSDVKLEKPKYPPHCEEKVITTT 72
D 1 MRLAALLLLLTARVDGSKCKSRGPKIRYSDVKLEKPKYPPHCEEKVITTT 72
Db 1 MRLAALLLLLTARVDGSKCKSRGPKIRYSDVKLEKPKYPPHCEEKVITTT 72

QY 73 KSVSRGQEHLPKLOSTKRFIKYNNANNEKRYVEE 111
D 73 KSVSRGQEHLPKLOSTKRFIKYNNANNEKRYVEE 111
Db 61 KSVSRGQEHLPKLOSTKRFIKYNNANNEKRYVEE 99

RESULT 4
Q9DFG4 PRELIMINARY; PRT; 100 AA.
AC Q9DFG4;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CXC-TYPE CHEMOKINE.
GN SCYB4.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasboreinae; Danio.
NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11025222;
RA Long Q., Quint E., Lin S., Ekker M.;
RT "The zebrafish scyba gene encodes a novel CXC-type chemokine with distinctive expression patterns in the vestibulo-acoustic system during embryogenesis,"
RL Mech. Dev. 97:185-186(2000).
DR EMBL; AF279919; AAG09819.1; -
SQ SEQUENCE 100 AA; 12016 MW; 274BE255A74F98B5 CRC64;

Query Match 57.1%; Score 335; DB 13; Length 100;
Best Local Similarity 54.6%; Pred. No. 7.2e-30;
Matches 53; Conservative 25; Mismatches 19; Indels 0; Gaps 0;

QY 14 RLTAALLLLLTARVDGSKCKSRGPKIRYSDVKLEKPKYPPHCEEKVITTT 73
D 1 RLTAALLLLLTARVDGSKCKSRGPKIRYSDVKLEKPKYPPHCEEKVITTT 73
Db 3 RCTAALLFLTAIVASLNTFAKCKCTKPKIRITDVQKLEIKPKHRYCOEKKMIFVME 62

QY 74 SVSRGEOEHCHPKLOSTRKFIKYNAMNEKRRVVE 110
 Db 63 NVSRFGOEYCLHPRLOSTRNVLKWKDKRHTFE 99

RESULT 5
 Q9DGL8 PRELIMINARY; PRT; 98 AA.

AC Q9DGL8; 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DE JUN-SUPPRESSED CHEMOKINE.
 GN JSC.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=FIBROBLAST;
 RA Hartl M., Bister K.;
 RT "Suppression of genes in jun-transformed avian fibroblasts."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF285876; AAC00529.1; -
 SQ SEQUENCE 98 AA; 11564 MW; 30D88E540AADD35B CRC64;

Query Match
 Best Local Similarity 54.9%; Score 322.5; DB 13; Length 98;
 Matches 60; Conservative 19; Mismatches 18; Indels 3; Gaps 2;

QY 13 MRLAALALLLLALYARVDSKCKSRKPKIRYSVVKLEMKPKYPHCEKMYITTT 72
 Db 1 MKLTLALLLVIAMCLASABGVKCKSRKPKIRFSNVAKLEKPRYPCVEEMITVL 60

QY 73 KVSRYNG-QEHCILPKLOSTRKFIKYNAMNEKRRVVE 111
 Db 61 -WTKVRGEODHCLNPKRONTVRLKMYRWKKEGRVYEE 98

RESULT 6
 Q9EP62 PRELIMINARY; PRT; 101 AA.

AC Q9EP62; 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DE CINC-2 ALPHA PRECURSOR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WISTAR; TISSUE=PERITONEAL CAVITY;
 RX MEDLINE=98236997; PubMed=9576061;
 RA Shibata F., Konishi K., Nakagawa H.;
 RT "Gene structure, cDNA cloning, and expression of rat cytokine-induced neutrophil chemoattractant 2 (GRO/CINC-2) gene."
 RT Cytokine 10;165-174(1998).
 DR EMBL: D87927; BAB12280.1; -
 DR EMBL: D87926; BAB12279.1; -
 DR InterPro: IPR001811; Chemokine_IL8.
 DR InterPro: IPR001089; Small_cytokine_CXC.
 DR Pfam: PF00048; IL8; 1
 DR PRINTS: PR00437; SMALLCYTKCXC.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
 DR SIGNAL.
 FT CHAIN 1 32 POTENTIAL.
 FT SIGNAL 33 101 CINC-2 ALPHA.

SQ SEQUENCE 101 AA; 11109 MW; D949D5712FE30909 CRC64;

Query Match
 Best Local Similarity 24.4%; Score 143.5; DB 11; Length 101;
 Matches 34; Conservative 19; Mismatches 31; Indels 13; Gaps 3;

QY 8 APPVSMRLAALALLLLALYARVDS-----KCKSRKPKIRYSVVKLEMKPKYP 60
 Db 2 APP-TRRLAALALLLLLMATSHQSPGVAVARELCQCLTKLPRVDFENIQSLVTPPG 60

QY 61 PHCEKMYITTTKVSRYNGOECHLPHKLOSTRKFIK 97
 Db 61 PCHQTEVIATLKD-----GEVCLNPAOPARLOKIIQ 92

RESULT 7
 Q28724 PRELIMINARY; PRT; 108 AA.

AC Q28724; 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-AUG-1999 (Tremblrel. 11, Last sequence update)
 DE GRO (PERMEABILITY FACTOR 2).
 GN RPF2.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NEW ZEALAND WHITE;
 RA Yoshimura T., Modi W.S.;
 RT "Isolation of novel GRO genes, and a phylogenetic analysis of the CXC chemokine subfamily in mammals."
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 43-108 FROM N.A.
 RC STRAIN=NEW ZEALAND WHITE;
 RX MEDLINE=95129889; PubMed=7828903;
 RA Johnson M.C., Goodman R.B. II, Kajikawa O., Wong V.A., Mongovin S.M., Martin T.R.;
 RT "Cloning of two rabbit GRO homologues and their expression in alveolar macrophages."
 RT Gene 151;337-338(1994).
 DR EMBL: U95808; AAB93924.1; -
 DR EMBL: I28933; AAB6975.1; -
 DR HSPF: P19875; IONK.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR InterPro: IPR001089; Small_cytokine_CXC.
 DR Pfam: PF00048; IL8; 1.
 DR PRINTS: PR00437; SMALLCYTKCXC.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
 DR SIGNAL.
 SQ SEQUENCE 108 AA; 11261 MW; 9C278041FC7A5BAD CRC64;

Query Match
 Best Local Similarity 21.9%; Score 128.5; DB 6; Length 108;
 Matches 32; Conservative 15; Mismatches 36; Indels 11; Gaps 2;

QY 8 APPVSMRLAALALLLLALYARVDS-----KCKSRKPKIRYSVVKLEMKPKYP 61
 Db 9 AAPSGRFLRTAMLLLLLLASRAAGAAALTELNCQCLQYVQGIHLKSLQKVLSPG 68

QY 62 HCEKMYITTTKVSRYNGOECHLPHKLOSTRKFIK 97
 Db 69 HCAQTEVIATLKS-----GEVCLNPAAPVWVKFLO 99

RESULT 8
 Q98T02 PRELIMINARY; PRT; 97 AA.

AC 099ME0;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE CXC CHEMOKINE RTCK1.
 GN RTCK1.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Fu W., Gong S., Chen W.;
 RT "Cloning and Characterization of a Novel Gene Coding the Homologous
 RT Gene to RTCK1."
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF349115; AAK30166.1;
 SO SEQUENCE 111 AA; 12159 MW; 8230226BC7C60A55 CRC64;

Query Match 14.9%; Score 87.5; DB 11; Length 111;
 Best Local Similarity 23.9%; Pred. No. 0.03;
 Matches 22; Conservative 22; Mismatches 37; Indels 11; Gaps 2;

OY 12 SMRLAALLLLALTYARVDS-----KCKSRKPKIRYSDVKLEMKPKYPCHEE 65
 DB 19 NLQVLSLLVALVPLANGKPDNNPTELRCRCTLGSLPLNSISRVNFRGACND 78
 OY 66 KMWITTKSVSRYGQEHCLPKLQSTKRFRK 97
 DB 79 VEVATLTKN-----GREVCIDPTAPMKIKIYK 105

RESULT 12
 ID 073912 PRELIMINARY; PRT; 104 AA.
 AC 073912;
 DT 01-AUG-1998 (TREMblrel. 07, Created)
 DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE K60 PROTEIN PRECURSOR (CXC CHEMOKINE K60).
 GN K60.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OX Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE-MACROPHAGE LIKE;
 RL Sick C.;
 RN Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20170941; PubMed=10704244;
 RA Sick C., Schneider K., Staeheli P., Melning K.C.;
 RT "Novel chicken CXC and CC chemokines."
 RL Cytokine 12:181-186(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Hughes S.M., Bumstead N.;
 RT "Mapping of a second ELR CXC chemokine to chicken chromosome four."
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Y14971; CAA75212.1;
 DR EMBL; AE277660; AAF86485.1;
 DR HSSP; P02775; ITVX.
 DR InterPro; IPR001811; Chemokine_IL8.
 DR InterPro; IPR001089; Small_cytokine_CXC.
 DR Pfam; PF00048; IL8; 1
 DR PRINTS; PRO0437; SMALLCYTKKCX.
 DR SMART; SM00199; SCY; 1.
 DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
 KW Signal.

FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 104 K60 PROTEIN.
 SO SEQUENCE 104 AA; 11199 MW; 83725AB91FE18B3D CRC64;

Query Match 14.7%; Score 86.5; DB 13; Length 104;
 Best Local Similarity 28.3%; Pred. No. 0.036;
 Matches 25; Conservative 15; Mismatches 38; Indels 13; Gaps 3;

OY 14 RLAAALLLLALTYARVDS-----KCKSRKPKIRYSDVKLEMKPKYPCHEE 65
 DB 4 KAVAAVALLLISMAAGKGAQAARSATLRCQCLETGHSKPIHPKLIQNVNLTPSGPCKN 63
 OY 66 KMWITTKSVSRYGQEHCLPKLQSTKRFRK 97
 DB 64 VEVATLTKN-----GREVCIDPTAPMKIKIYK 90

RESULT 13
 ID 09PTF8 PRELIMINARY; PRT; 93 AA.
 AC 09PTF8;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE CC CHEMOKINE CCL1.
 GN CCL1.
 OS Brachydanio rerio (zebrafish) (Zebra danio).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Ostariophysi;
 OX Cypriniformes; Cyprinidae; Rasbora; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tseng S., Rollins B.J.;
 RT "Chemokines and chemokine receptors in zebrafish."
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF201450; AAF17560.1;
 DR InterPro; IPR001811; Chemokine_IL8.
 DR Pfam; PF00048; IL8; 1.
 DR SMART; SM00199; SCY; 1.
 SO SEQUENCE 93 AA; 10776 MW; 17C9B5309903ED7 CRC64;

Query Match 14.7%; Score 86; DB 13; Length 93;
 Best Local Similarity 29.4%; Pred. No. 0.037;
 Matches 25; Conservative 15; Mismatches 27; Indels 18; Gaps 3;

OY 22 LLLALLTY-----ARYDSKCKSRKPKIRYSDVKLEMKPKYPCHEE 72
 DB 8 LLLVCFITLITDNKGAAIPFCCLSVLRIRPKRVLRVRYEVDTSCHCEIKALLIL-- 65
 OY 73 KSVSRRYRGQEHCLPKLQSTKRFRK 97
 DB 66 ----HFKKKKCAHPKLE--RFLK 83

RESULT 14
 ID 09XSX5 PRELIMINARY; PRT; 101 AA.
 AC 09XSX5;
 DT 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE INTERLEUKIN-8.
 OS Felis silvestris catus (Cat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Straubinger A.F., Simpson K.W., Straubinger R.K.;
 RT "Feline Interleukin-8 mRNA."

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF158598; AAD40323.1; .
 DR HSSP: P10145; 11KM.
 DR InterPro: IPR001811; Chemokine_IL8.
 DR InterPro: IPR001089; Small_cytokine_CXC.
 DR Pfam: PF00048; IL8; 1.
 DR PRINTS: PR00437; SMALLCYTKCXC.
 DR SMART: SM00199; SCY; 1.
 DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
 DR SEQUENCE 101 AA; 11165 MW; 690D97F13EF79170 CRC64;

Query Match 14.2%; Score 83.5; DB 6; Length 101;
 Best Local Similarity 28.0%; Pred. No. 0.076; Indels 17; Gaps 5;
 Matches 28; Conservative 19; Mismatches 36;

QY 15 LLAALLLLLL--ALTYARDGS--KCKCSRK-----GPKIRYSDVKLEMKPKYPHCEEK 66
 DB 9 LLAEMLSAALCEAAVLRSISSELRCCCTKTHSTPPNPKL----IKELTVIDSGPHCENS 64
 QY 67 MVIITTKSVSRYGQEHCLHPKLOSTKRFILKYNANNEKR 106
 DB 65 EII-----KLVNGKEVCLDPKQKQVQKVEIFLKKAEKQ 99

RESULT 15

ID Q68398 PRELIMINARY; PRT; 117 AA.
 AC Q68398;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
 DT 01-NOV-1998 (TREMblrel. 08, last annotation update)
 DE ORF UL146.
 OS Human cytomegalovirus.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Cytomegalovirus.
 OX NCBI_TaxID=10359;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-TOLEDO;
 RX MEDLINE=96099416; PubMed=8523595;
 RA Cha T.A., Tom E., Kemble G.W., Duke G.M., Mocarski E.S., Spaete R.R.;
 RT "Human cytomegalovirus clinical isolates carry at least 19 genes not
 found in laboratory strains."
 RL J. Virol. 70:78-83(1996).
 DR EMBL: U33331; AAB5885.1; .
 DR SEQUENCE 117 AA; 13658 MW; E37A805502A9A0A4 CRC64;

Query Match 14.2%; Score 83.5; DB 12; Length 117;
 Best Local Similarity 27.5%; Pred. No. 0.088;
 Matches 30; Conservative 15; Mismatches 33; Indels 31; Gaps 6;

QY 13 MRLAALALLLLALTYARYDGS--KCKC-SRGP--KIRYSDVKLEMKPKYPHCEEK 67
 DB 1 MRLIFGALLIFLAVYVYENGTELRCCLHRKWPKNKILGNV-WLHRDPGPGCDK-- 57
 QY 68 VIITTKSVSRYGQEHCLHPK-----LOSTKRFILKYNANNEKR 106
 DB 58 -----NEHLIYPDGRRKPPGPGVCLSPDHLFSKWLDKHNDNR 93

Search completed: January 29, 2002, 16:05:16
 Job time: 102 sec

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	1640.4	97.4	1677	6	AX136401	AX136401 Sequence
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3	1179.2	70.0	108123	9	AC034206	AC034206 Homo sapi
4	1177.2	69.9	134506	9	AC005728	AC005728 Homo sapi
5	1175.6	69.8	79970	2	AC011428	AC011428 Homo sapi
6	1175.6	69.8	159420	2	AC009017	AC009017 Homo sapi
7	1163.6	69.1	81811	2	AC063961	AC063961 Homo sapi
8	1092.2	64.8	1630	6	AX013119	AX013119 Sequence
9	976.2	57.9	1962	6	AX011661	AX011661 Sequence
10	976.2	57.9	1962	6	AX013598	AX013598 Sequence
11	872.6	51.8	1962	6	AX011661	AX011661 Sequence
12	872.6	51.8	1962	6	AX013598	AX013598 Sequence
13	733.4	43.5	1845	10	AB041614	AB041614 Sequence
14	727.2	43.2	1663	10	AF144754	AF144754 Mus muscu
15	709.6	42.1	1884	10	AF192557	AF192557 Mus muscu
16	582.2	34.5	582	9	BC003513	BC003513 Homo sapi
17	580.3	34.4	592	6	AX136574	AX136574 Sequence
18	550.4	32.7	584	6	AX136715	AX136715 Sequence
19	439.6	26.1	463	9	AF106911	AF106911 Homo sapi
20	435.6	25.9	461	6	AR071210	AR071210 Sequence
21	386.2	22.9	386	9	AF073957	AF073957 Homo sapi
22	368.2	21.8	752	10	AF252873	AF252873 Mus muscu
23	367.2	21.8	533	10	AF352785	AF352785 Mus muscu
24	355.4	21.1	504	10	AF152377	AF152377 Mus muscu
25	354.2	20.9	354	9	HUM2D6C06	HUM2D6C06 Homo sapi
26	352.8	20.9	1630	6	AX013119	AX013119 Sequence
27	299.8	17.8	351	5	AF258786	AF258786 Mus muscu
28	150.8	8.9	1517	10	AF285876	AF285876 Gallus ga
29	127.7	7.5	128	11	G26440	G26440 human SMS T
30	122.8	7.3	1748	5	AF279919	AF279919 Danio rer
31	76.4	4.5	150	11	G59717	G59717 SHGC-130465
32	75.4	4.5	150	11	G42932	G42932 WIAR-209-ST
33	70.6	4.2	7218	6	I66494	I66494 Sequence 14
34	60.6	3.6	64809	2	AC091023	AC091023 Homo sapi
35	60.2	3.6	648221	2	PFM4L13P3	AL049184 Plasmodiu
36	60.2	3.6	4596	3	AF310896	AF310896 Dictyoste
37	59.6	3.5	771	9	BC000608	BC000608 Homo sapi
38	59.6	3.5	167277	2	AC025318	AC025318 Homo sapi
39	59.4	3.5	840	8	CNS0180K	AL110675 Botrytis
40	59.4	3.5	175352	2	AC092491	AC092491 Homo sapi
41	59.2	3.5	181831	2	AP003400	AP003400 Homo sapi
42	59.2	3.5	916	9	BC002516	BC002516 Homo sapi
43	58.8	3.5	166025	2	AC036200	AC036200 Homo sapi
44	58.4	3.5	132910	2	AC016342	AC016342 Homo sapi
45	58.4	3.5	223538	2	AC087150	AC087150 Mus muscu

ALIGNMENTS

RESULT	1
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LOCUS	AXI36401 1677 bp DNA
DEFINITION	Sequence 323 from Patent EP1067182.
ACCESSION	AXI36401
VERSION	AXI36401.1 GI:14272805
KEYWORDS	.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1677)
AUTHORS	Ota,T., Isegaki,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
TITLE	Secretory protein or membrane protein
JOURNAL	Patent: EP 1067182-A 323 10-JAN-2001;
FEATURES	Helix Research Institute (JF) Location/Qualifiers 1..1677

AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
 TITLE Direct Submission
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 108123)
 AUTHORS DOE Joint Genome Institute.
 TITLE Direct Submission
 JOURNAL Submitted (05-APR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 REFERENCE 3 (bases 1 to 108123)
 AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
 TITLE Direct Submission
 JOURNAL Submitted (21-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 REFERENCE 4 (bases 1 to 108123)
 AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
 TITLE Direct Submission
 JOURNAL Submitted (20-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 COMMENT On Jun 21, 2001 this sequence version replaced gi:9256720.
 Draft Sequence Produced by DOE Joint Genome Institute
 www.jgi.doe.gov
 www.shgc.stanford.edu
 Quality: Phrap Quality >=40 99.5% of Sequence;
 Estimated Total Number of Errors is 0.2.
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 SHGC-130469 G59717.
 Location/Qualifiers
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 1. 108123
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="5"
 /clone="CTC-321K16"
 BASE COUNT 27996 a 23419 c 26053 g 30655 t
 ORIGIN
 Query Match 70.0%; Score 1179.2; DB 9; Length 108123;
 Best Local Similarity 99.7%; Pired. No. 1.5e-217;
 Matches 1192; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 962 gctgcacaggctcctcgtggtctatgagccggtcacagctcagtgtaactccacagtg 1021
 Db 17100 GCTGCCAGGGCTCTCCTGGGCTATAGCGGTCACAGCCTCAGTGTGACCTCACAGTTGG 17041
 QY 1022 cccctgtacccgagcaagcaggaagcgtctctctgcatctgtctctcgtgaactcaag 1081
 Db 17040 CCCCTGTAGCGGGGCAACAGAGAGAGTCTGTGATCTGTCTGTGAGGAACCTCAAG 16981
 QY 1082 ttgtgtccagaagaaatgctctcatcccccctgtgtaatttttcacacccctagaa 1141
 Db 16980 TTTGGTCCAGAAAAAATGCTCTTATTCCTCCCTGGTTAATTTTACACACCTTAGAA 16921
 QY 1142 acattccaagatcctgtgatgagcagaacaatgatcccttaagaagtggtggtctt 1201
 Db 16920 ACATTTCAGAGTCTCTGTGATGCGCAGCAATATGCTTAAAGAGGTGGGCTCTT 16861
 QY 1202 cccaacgtgagattcttgaaagtgltcacaggttcaatattatgtctcagaagcatgt 1261
 Db 16860 CCCAAGCTGAGGATTTTGAAAGGTTTCAGAGTTCATATTTAATGCTTCAGAAAGCATGT 16801
 QY 1262 gagggtcccaacactgtcagcagaacacttgaggaaacttaaatatataatgatac 1321
 Db 16800 GAGGTTCCCAACACTGTGACGCAAAAACCTTAGAGAAAACTTAATAATATATGATACAT 16741
 QY 1322 ggcacatacacagctacagacacacatctgttgcaaggaggaacacttcaaacatgt 1381
 Db 16740 GCGCAATACACAGCTACAGACACACATCTGTGCAAGGAGAAAACTTCAACAGATGT 16681
 QY 1382 tcttccctcacacaagaacacatgacagtaactaaagcatatattgtatcccatg 1441
 Db 16680 TCTTTCCCTCACACACAGAACATGACAGTAAAGCAATATATTTGTGATTCCTCATG 16621
 QY 1442 taattctcaatgtaaacagtgagctcctcttcgaaagctaaagatgacatgcgccc 1501
 Db 16620 TAATTCTCAATGTTAAACAGTGCGCTCTTCTTGAAAGCTAAGATGACATGCGCCCT 16561
 QY 1502 ttcctcgtacatacaccttaagaagcccccctcacacactgcccccatatagcc 1561
 Db 16560 TTCCCTGTACATATACCTTAAAGAGCCGCCCTCACACACTGCCCCAGTATATGCC 16501
 QY 1562 gcaattgactcgtgtatataatgctatgacatgcaagaacatgacatgcatgag 1621
 Db 16500 GCATTGTACTGCTGTATATATGCTATGATGTCACAAACCATATACATTTGATGAG 16441
 QY 1622 gttcatattcttttaagatgaaagtaataatatttgaatgaaatgaaatgaaatg 1677
 Db 16440 GTTTCATATTCTTTCTAAGATGAAAGTATATATTTTGAATGTTACCAAAA 16385

RESULT 4
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 LOCUS Homo sapiens chromosome 5, BAC clone 7g12 (LBNL H126), complete
 DEFINITION
 ACCESSION AC005738 AC004619 L81405 L81406 L81678 L81679 L81680 L81861
 L81862 AC001042 AC001043 AC001520
 VERSION AC005738.1 GI:3687213
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 134506)
 AUTHORS Kimmerly, W., Bondoc, M., Cheng, J., Connolly, K.S., Gunning, K.M.,
 Kader, K., Miguel, T., Miller, C., Pitluch, S., Pollard, M.,
 Rojeski, H., Subramanian, S. and Martin, C.H.
 TITLE Sequencing of human chromosome 5
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 134506)
 AUTHORS Rieke, D.O.
 TITLE Large Scale Sequence Analysis and Annotation with the Sequence
 Comparison Analysis (SCAN) System
 JOURNAL Unpublished


```

REFERENCE 3 (bases 1 to 134506)
AUTHORS Kimmery,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,
Rader,K., Miguel,T., Miller,C., Piltuck,S., Pollard,M.,
Rojas,H., Subramanian,S. and Martin,C.H.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-1998) Human Genome Center, DOE Joint Genome
Institute, Lawrence Berkeley National Laboratory, MS 74-157,
Berkeley, CA 94720, U.S.A.
REFERENCE 4 (bases 1 to 134506)
AUTHORS Ricke,D.O.
TITLE Direct Submission
JOURNAL Submitted (13-OCT-1998) Los Alamos National Laboratory, DOE Joint
Genome Institute, T443, HRL-1, LS-3, MS M888, Los Alamos, NM 87545,
USA
REFERENCE 5 (bases 1 to 134506)
AUTHORS Ricke,D.O.
TITLE Direct Submission
JOURNAL Submitted (20-OCT-1998) Los Alamos National Laboratory, DOE Joint
Genome Institute, T443, HRL-1, LS-3, MS M888, Los Alamos, NM 87545,
USA

COMMENT Sequence submitted by:
FEATURES DOE Joint Genome Institute.
LOCATION/Qualifiers
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VERSION AC011428.3
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 79970)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 5
JOURNAL Unpublished
PUBLISHED 2 (bases 1 to 79970)
DOE Joint Genome Institute.
REFERENCE 2 (bases 1 to 79970)
DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (06-OCT-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT On Nov 15, 2000 this sequence version replaced gi:1660400.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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Project Information

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Center Project Name: 1189149, H122
Center Clone name: XXPI-380H11

Summary Statistics

Consensus quality: 76910 bases at least Q40
Consensus quality: 78432 bases at least Q30
Consensus quality: 78894 bases at least Q20
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Estimated insert size: 79670; sum-of-coverage estimation
Quality coverage: 7.19 in Q20 bases; pulse field gel estimation
Quality coverage: 6.49 in Q20 bases; sum-of-coverage estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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DEFINITION 26 unordered pieces.
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VERSION AC009017.4 GI:13699469
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 159420)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 5
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 159420)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT On Apr 20, 2001 this sequence version replaced gi:1178048.
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Center: Joint Genome Institute
Center Code: JGI

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REFERENCE	1 (bases 1 to 1630)		
AUTHORS	Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and Pilarsky,C.		
TITLE	Human nucleic acid sequences of endometrium tumour tissue		
JOURNAL	Patent: WO 9954461-A 59 28-Oct-1999;		
	SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN		
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Db	1252	AGAAA	ACTT	AAAAA	TATATAT	ATATAT	ATATAT	ATATAT	ATATAT	ATATAT	1311
Qy	1355	gaca	ag	gg	aaaa	ac	ctt	taag	cat	gttctt	1414
Db	1312	GACA	AGG	GA	AAAC	CTTCA	AA	GCAT	GT	TTCTT	1371
Qy	1415	aaag	ca	at	ata	lata	ttt	gt	at	cccat	1474
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Qy	1475	toga	ag	at	ga	at	ga	at	ga	at	1534
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Qy	1535	toca	ac	ac	at	ctt	cccc	ag	at	ata	1594
Db	1492	TCCA	AC	AC	CTG	CCCCC	CCAG	TATAT	GCGCG	ATATG	1551
Qy	1595	gtc	aga	aa	cc	at	lga	at	lga	at	1654
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Qy	1655	aata	tatt	tt	ga	at	at	at	at	at	1711
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RESULT	9				
LOCUS	AX011681				
DEFINITION	Sequence	1962 bp	DNA	PAT	06-SEP-2000
ACCESSION	AX011681				
VERSION	AX011681.1	GI:998205			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 1962) Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and Pliarsky,C.				
TITLE	Human nucleic acid sequences obtained from pancreas tumor tissue				
JOURNAL	Patent: WO 995858-A-77 04-NOV-1999; SCMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN BERND (DE); ROSENTHAL ANDRE (DE); METZGEN GES FUER GENOMFORSCHUN (DE); PLIARSKY CHRISTIAN (DE)				
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ORIGIN					

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OY	635	aagacacaatttatattgttataggaacttttaacaaagtgtaatttttaacattt	694	
DB	939	AAGACCAAAATTTATATATTTGTTATGAGCACTTTTACCAAGCGTAGTTTAACTTTT	998	
OY	695	atagctcgctgcgaagagcttcacagatggaagaccatctctctgtgctcagacttca	754	
DB	999	ATAGCTGCGTGGGAAAGCGCTTCAGATGGAGACCATCTCTCTTGTGCTCCAGACTTCA	1058	
OY	755	tcaacggctgcgtttttatcaaaaaaggggaaactcatgctcttctctttaaanaatgct	814	
DB	1059	TCACAGGCTGCTTTTATATCAAAAAAGGGGAAACATCATGCTTTCTTTAAAAATGCT	1118	
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DB	1119	TTTTGTATTTTCCATAGCTACATCTATCATCTGTGACCTTTATTAAGGCGCCGGAGGAA	1178	
OY	875	atgagcttggtggacaacattcatatgacagtgtgtctccattctcagcttgggaagcttc	934	
DB	1179	ATGACCTTGGTGGACACATTTTCATTGCAAGTGTGCTCCATCTCTTAAGCTTGGGAGCTTCC	1238	
OY	935	gcttagaaggtctcctggcgcctcggcagcagctggcgaagggtctctccctgggctatagccggt	994	
DB	1239	GCTTAGAGGTCTCGGCGCCTCGGCAAGCTGCGCAAGGCGCTCTCTCGGGGCTTATGGCGGT	1298	
OY	995	cacaagcctcagtgtagctccacagcagcgccctgtagcgcggcgaagaagagcagctctc	1054	
DB	1299	CACAGCCTCAGGTGACTTCACAGTGGGCCCTGTAGCGCGGCAACAGSAGCAGGCTCT	1358	
OY	1055	ctgactcgtctctcgaaggaatcaagtttggttgtgccagaanaatgtgcttcatctccc	1114	
DB	1359	CTGACTCTGTTCTCGAAGGAACCTCAAGTTTGGTTCCCAAAAAAGTGTCTTATCTCCCC	1418	
OY	1115	cttggttaattttaaacaaccctaggaanaacattccaagaatcctgtgatgccaagaat	1174	
DB	1419	CTGGTATTTTTCACACCCTCAGGAAACATTTCCAAAGTCTGTGATGGCGAGCAAAAT	1478	

QY	1175	gaccttcaagaagctctggagctcttcccaacctgaggattctcgaaggttcaagct	1234
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DEFINITION	AY013598 1962 bp DNA
ACCESSION	Sequence 541 from Patent WO9954461.
VERSION	AY013598
KEYWORDS	AY013598.1 GI:10040378
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Elkayrola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1962)
AUTHORS	Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and Pilarsky,C.
TITLE	Human nucleic acid sequences of endometrium tumour tissue
JOURNAL	Patent: WO 9954461 A 541 28-OCT-1999;
FEATURES	SCHEMTT ARMIN (DE): SPECHT THOMAS (DE): DAHL EDGAR (DE): HINZMANN BRAND (DE): ROSENTHAL ANDRE (DE): METAGEN GES FUER GENOMFORSCHUN (DE): PILARSKY CHRISTIAN (DE) Location/Qualifiers 1..1962 /organism="Homo sapiens" /db_xref="taxon:9606"
BASE COUNT	547 a 440 c 431 g 544 t
ORIGIN	

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OY	635	aagacacaaattatatgtttaagcacttttaccaaagtcagttttacattt	694	
	939	AAGACACAAATTATATATTGTATTATGACACACTTTTACCACAGGTCAGTTTTTAAATTTTT	998	
OY	695	atagctgctgcgaagagcttcagaatggaaaccactctctcgtctccagaactca	754	
	999	ATAGCTGGTGCGAAGAGGCTTCCAAATGGGAAACCACATCTCTCTTGCTGCCAGACTTCA	1058	
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LOCUS AX011681
DEFINITION Sequence 77 from Patent WO955858.
ACCESSION AX011681
VERSION AX011681.1 GI:9998205
KEYWORDS
SOURCE
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1962)
AUTHORS Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and
Pillarsky,C.
TITLE Human nucleic acid sequences obtained from pancreas tumor tissue
JOURNAL Patent: WO 955858-A 77 04-NOV-1999; DAHL EDGAR (DE); HINZMANN
SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN

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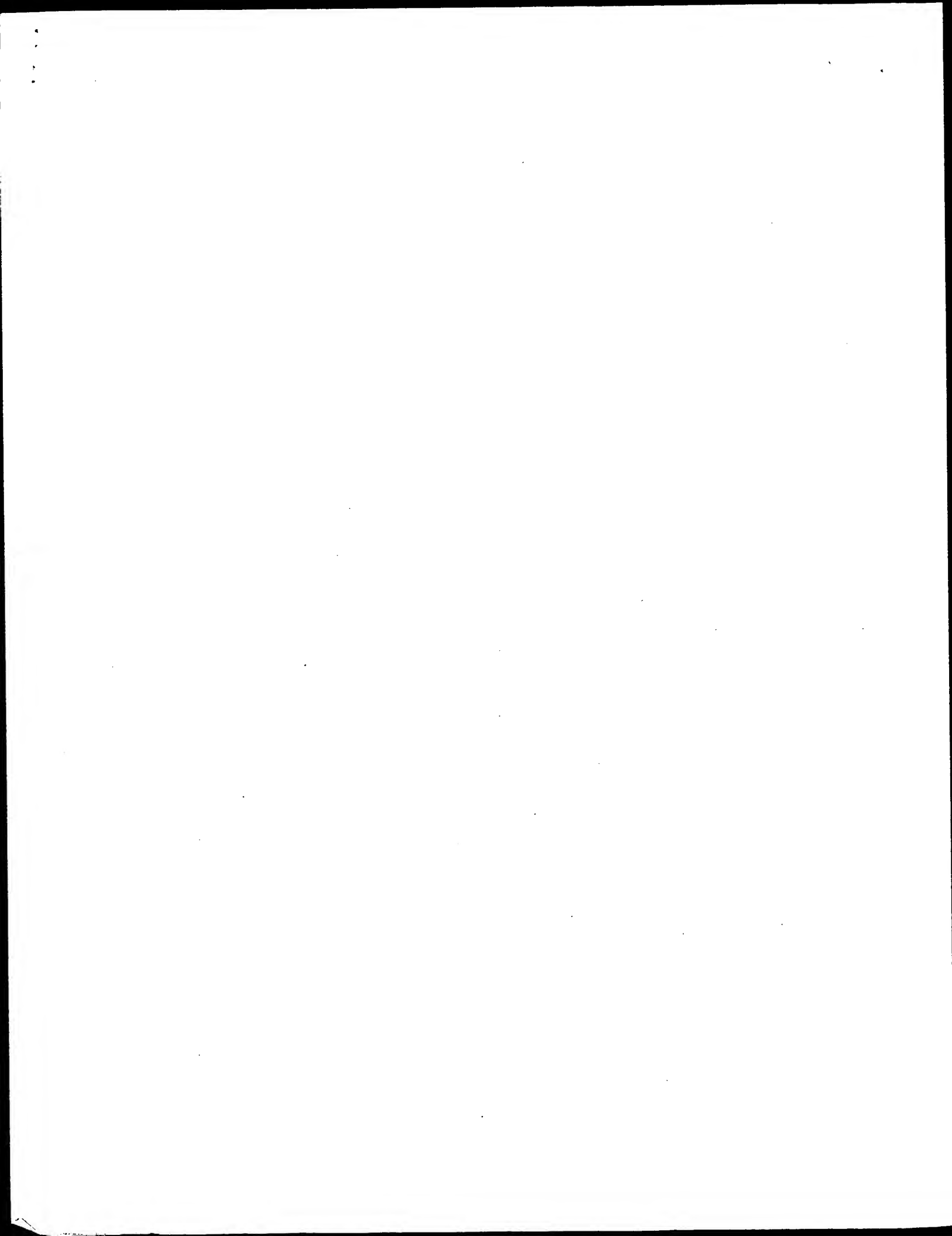
BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GBS FUER GENOMFORSCHUN
(DE); PILLARSKY CHRISTIAN (DE)
FEATURES
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BASE COUNT 547 a 440 c 431 g 544 t
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RESULT	15
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DEFINITION	Mus musculus kidney-expressed chemokine CXC (Kec) mRNA, complete cds.
ACCESSION	AFI92557
VERSION	AFI92557.1 GI:6103732
KEYWORDS	.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eumariyola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 1884)
TITLE	Mang, L., Deng, L., Raikwar, N., Sahota, A. and Tischfield, J.A.
JOURNAL	Identification of a kidney-expressed chemokine (KEC), a member of the CXC family, that is selectively elevated in aprt knockout mice Unpublished
REFERENCE	2 (bases 1 to 1884)
AUTHORS	Mang, L., Deng, L., Raikwar, N., Sahota, A. and Tischfield, J.A.
TITLE	Direct Submission
JOURNAL	Submitted (06-OCT-1999) Genetics, Rutgers University, 604 Allison Road, Piscataway, NJ 08854-8082, USA
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QY	611	aaagccttccttcctccagagcaalagaacaaatatatctgtctatgaagcactcttc	670
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QY	898	ttgacagttgtctcatctaccatagcttggaagcttcgcgtctgactgagctgcgcgcg	957
Db	1048	CAGACATACGTCTCCGCTCCAGGCTTACAAAGCTTCCGCTCAGAGAGACCTCGCGGCTCG	1107
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PR	30-JUL-1998;	98US-0094651.
PR	11-SEP-1998;	98US-0100038.

AA
PA (GETH) GENENTECH INC.

xx Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
PI

XX
DR WPI; 1999-551358/46

P-P50B; AA141/33.
 DR
 XX

PT useful for treating blood coagulation disorders, cancers and cellular

XX
f1
QUALIFICATION INSTRUCTORS

CLASSIC 2, FIG 140, 500PP, ENG-14000.

CC and their polynucleotides. The nucleotide sequences are useful as

of antisense sequences. They can also be used to create transgenic

disorders, depending on their function. Diseases that may be treated

disorders. They may also be used to raise antibodies. AA233891 to

polypeptide sequence given in the exemplification of the present

[illegible]

Query Match	100.0%;	Score 1685;	DB 20;	Length 1685;
Query	100.0%;	Score 0;	DB 0;	Length 0;

Matches 1685; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcggagacaagcgcagagcgcacgcccctggcatccaccgacgg 60

Db 1 gcggaagcaagcgcagcgcagcgcacagacagccctggtcatccaccgaagg 60

61 cgcagccgagccagcagagccggaagcgcgcccggcagagaagaagccgagcagagct 120

Db 61 cgccagccggaagccagcaagcgcgcgcccggcagagaaagccgagcagagct 120

QY 121 gggtgagctctccggagccgctccgacgggccaagcgccctcccatgtccctgctccc 180

Db 121 gggtgagctctccgggagccgctccggaaggagccctcccatgtccctgctccc 180

QY 181 acgcccgcgccctccggtcagcatgagctccctgagcgccgcgctgtctccctgtctgtct 240

Db 181 acgcccgcgccctccggtcagcatgaggcttcctggcgccgcgcctgcctccctgcctgcct 240

QY 241 ggcgctgtacaccgcgcgtgtggacgggtcccaatgcaatgtcctccggaagggaccaca 300

Db 241 ggcgctgtacaccgcgcgtgtggaacgggtcccaalgcagtcgctcccgaaagggaccaca 300

QY 301 gatccgctacagcgacgtgaaagaagcttggaaatcgaagccaatgacccgaagcgcgagga 300

Dd 301 gatccgctacagcgacgctggaalgaagccaaagcaccgcacccgcagga 300

QY 361 gaagatggttatacattcacccacgaagcgctgctcgaagctaccgagggccagggagggccacggccgccc 420

Db 361 gaagatggttatcatcacccaccaagagcgcggtccaggtaccgaggtccaggtaccgtccc 420

QY 421 gcaccccaagctgcagagcaccacagcgcctccalcacagcggccacaacgcccggaaacgagaa *uu

Dd 421 gcacccgaagctgcagagcaccgaagcgcllcalcaaglyg laccaagcc agyaacyaa *00

QY 481 gcgcagggtctcactgaagaaatagggcgaaaaacccagaaggggaaaaccaccaaaccaagccg

D5 481 gcgcagggtcctacgaaagaaacagggcgaadaaaccccaaacccagccg 540

541 ggagactctgcagaagcactctgcagatcaaaaaaaaaaaaaaaaaaaaaaaaaa 00


```

Db      541 gggacttgcgaagagcttgcagattaaataaaaaaataaaaaaataaaaaa
QY      601 aaaaaaaaaaagcttcttcttcacagcgaataagacacaaatataatgttata
Db      601 aaaaaaaaaaagcttcttcttcacagcgaataagacacaaatataatgttata
QY      661 agcattttaccacagctcagttttataattatagctgcgtgcgaaggcttcaga
Db      661 agcattttaccacagctcagttttataattatagctgcgtgcgaaggcttcaga
QY      721 tgggaagaccatctctctgtgtgcacagctcacaagctgcgtctttatcaaaag
Db      721 tgggaagaccatctctctgtgtgcacagctcacaagctgcgtctttatcaaaag
QY      781 ggaacacatagcttcttctttaaataatgcttttgatttgcattgcacgtacaa
Db      781 ggaacacatagcttcttctttaaataatgcttttgatttgcattgcacgtacaa
QY      841 tacatctgagcttataagcgccgggaggaacaatgagcttgcgtgcacatttcat
Db      841 tacatctgagcttataagcgccgggaggaacaatgagcttgcgtgcacatttcat
QY      901 cagttgtctcatcttctctagcttgggaagcttcgccttagaggtccgtgcac
Db      901 cagttgtctcatcttctctagcttgggaagcttcgccttagaggtccgtgcac
QY      961 agctgcacgggctctcctgcgtttagcgcgtacacagcttgcagcttgcacag
Db      961 agctgcacgggctctcctgcgtttagcgcgtacacagcttgcagcttgcacag
QY      1021 gccctgttagcgggacaggaagagtgctctgcacgtcttgcacgaagacaa
Db      1021 gccctgttagcgggacaggaagagtgctctgcacgtcttgcacgaagacaa
QY      1081 gtttgcgtgcgaataatgtgtcttcatcccccgtgttaattttacacacctagga
Db      1081 gtttgcgtgcgaataatgtgtcttcatcccccgtgttaattttacacacctagga
QY      1141 aacatttccaagaatcctgtgtagcgaagaacaatgactttaaagaagtggtgggtct
Db      1141 aacatttccaagaatcctgtgtagcgaagaacaatgactttaaagaagtggtgggtct
QY      1201 tcccaacgtgaggttcttcgaaggttcacaggttcaatattatgcttcgaagcag
Db      1201 tcccaacgtgaggttcttcgaaggttcacaggttcaatattatgcttcgaagcag
QY      1261 tgaagttcccaacactgtcagcaaaaaccttaggagaaaacttaaaatataatga
Db      1261 tgaagttcccaacactgtcagcaaaaaccttaggagaaaacttaaaatataatga
QY      1321 tgcgcaatacagaagctacagacacatctgttgaacagggaaaaaccttcaagcag
Db      1321 tgcgcaatacagaagctacagacacatctgttgaacagggaaaaaccttcaagcag
QY      1381 ttccttccctccacaacagaacatgctagtaacgaatataatltgtatcccat
Db      1381 ttccttccctccacaacagaacatgctagtaacgaatataatltgtatcccat
QY      1441 gtaattcttcaatgttaaacagtgacgtctcttgcgaagcttaagaatgacatgc
Db      1441 gtaattcttcaatgttaaacagtgacgtctcttgcgaagcttaagaatgacatgc
QY      1501 tttccctgtatataatagccttaagaagccctccacaacactgcctcccgatata
Db      1501 tttccctgtatataatagccttaagaagccctccacaacactgcctcccgatata
QY      1561 cgcattgtactgcgtgtgtatatatgtatgtacatgtcagaacacattagcatgtaga
Db      1561 cgcattgtactgcgtgtgtatatatgtatgtacatgtcagaacacattagcatgtaga
QY      1621 ggtttcattcttcttcaagaatggaagtaataataatatttgaaatgtaaaaaaa

```

```

Db      1621 ggttcataatcttcttcaagatggaagtaataataatatttgaaatgtaaaaaaa
QY      1681 aaaaa 1685
Db      1681 aaaaa 1685

RESULT 2
AAC78551
ID AAC78551 standard; cDNA; 1685 BP.
XX
AC AAC78551
XX
DE 08-FEB-2001 (first entry)
XX
Human PR0273 (UNQ240) nucleotide sequence SEQ ID NO:369.
XX
Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;
XX
expressed sequence tag; detection: cancer; ss.
XX
Homo sapiens.
XX
PM W0200053756-A2.
XX
PD 14-SEP-2000.
XX
PF 18-FEB-2000; 2000WO-US04341.
XX
PR 08-MAR-1989; 99WO-US05028.
PR 12-MAR-1989; 99US-0123957.
PR 29-MAR-1989; 99US-0126773.
PR 21-APR-1989; 99US-0130232.
PR 28-APR-1989; 99US-0131445.
PR 14-MAY-1989; 99US-0134287.
PR 23-JUN-1989; 99US-0141037.
PR 26-JUL-1989; 99US-0145698.
PR 29-OCT-1989; 99US-0162506.
PR 30-NOV-1989; 99WO-US28313.
PR 02-DEC-1989; 99WO-US28551.
PR 02-DEC-1989; 99WO-US28565.
PR 16-DEC-1989; 99WO-US30095.
PR 30-DEC-1989; 99WO-US31243.
PR 30-DEC-1989; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Bolstein D, Desnoyers L, Eaton DJ,
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gertlisen ME,
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ,
PI Kiljavin JU, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA,
PI Shelton DJ, Stewart TA, Tumas D, Williams PM, Wood WI;
XX
WP1: 2000-611443/58.
DR P-PSDB; AAB44295.
XX
PT Novel PRO polypeptides and polynucleotides used in detection methods,
XX
to target bioactive molecules to specific cells, and to modulate
XX
cellular activities -
XX
PS Claim 2; Fig 148; 636pp; English.
XX
AC AAC78458 to AAC78599 represent polynucleotide and EST (expressed
CC
sequence tag) sequences which encode secreted or transmembrane PRO
CC
polypeptides. The PRO polynucleotides and polypeptides have cytosolic
CC
activity. The polynucleotides and polypeptides can be used for detecting
CC
the presence of PRO polypeptides in samples, for linking bioactive
CC
molecules to cells and for modulating biological activities of cells,
CC
using the polypeptides for specific targeting. The polypeptide targeting
CC
can be used to kill the target cells, e.g. for the treatment of cancers.
CC
The polypeptide pairs provide specific targeting of bioactive molecules

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[illegible]

QY	961	agcgccacagggctctctcgtggttattgcccgttcacagcctccagtgtgactccacagtg	1020
Db	961	agctgcacagggctctctcgtggttattgcccgttcacagcctccagtgtgactccacagtg	1020
QY	1021	gccccttaagccgggcaagcagcagcagctctctcgtcactcgtctctcttgaggactcaa	1080
Db	1021	gccccttaagccgggcaagcagcagcagctctctcgtcactcgtctctcttgaggactcaa	1080
QY	1081	gtttgtgtgccagaanaaatgtgtctcatctcccccgtgttaattttcacacccctaggaa	1140
Db	1081	gtttgtgtgtccagaanaaatgtgtctcatctcccccgtgttaattttcacacccctaggaa	1140
QY	1141	aaactttccaaagatccctgtatgtgcgagcacaattgtcctttaagaagaagtggttgagttt	1200
Db	1141	aaactttccaaagatccctgtatgtgcgagcacaattgtcctttaagaagaagtggttgagttt	1200
QY	1201	tcccaacctgaggaattctcttaagaaggttcacaggtttcaatatattaaatgtcttcagaagcag	1260
Db	1201	tcccaacctgaggaattctcttaagaaggttcacaggtttcaatatattaaatgtcttcagaagcag	1260
QY	1261	tgaagttcccaacaacatgtcagcacaacaccttaaggagaaacttaanaatatatgaataca	1320
Db	1261	tgaagttcccaacaacatgtcagcacaacaccttaaggagaaacttaanaatatatgaataca	1320
QY	1321	tgcgcatacacagctacagacacacactctgtttgcaagggaanaaccttcanaagcatgt	1380
Db	1321	tgcgcatacacagctacagacacacactctgtttgcaagggaanaaccttcanaagcatgt	1380
QY	1381	ttcttccctccacacacacagcaacatgacgtactaaagaacatatattgtgattccocat	1440
Db	1381	ttcttccctccacacacacagcaacatgacgtactaaagaacatatattgtgattccocat	1440
QY	1441	gtaattcttaabgtttaaagaagtcagctcctcttctgaagaagtaagatgacatgagcc	1500
Db	1441	gtaattcttaabgtttaaagaagtcagctcctcttctgaagaagtaagatgacatgagcc	1500
QY	1501	ttctcctcgtacataccctttaagaagcgcctctccacacacatctgccccacgtatattgc	1560
Db	1501	ttctcctcgtacataccctttaagaagcgcctctccacacacatctgccccacgtatattgc	1560
QY	1561	cgcattgtactgctgtgttattatgctatgtacatgttcagaacaaccttagcattgcagca	1620
Db	1561	cgcattgtactgctgtgttattatgctatgtacatgttcagaacaaccttagcattgcagca	1620
QY	1621	ggtttccatattctcttccaagaatggaagtaataaataattttggaatgttaaaaaaaaaa	1680
Db	1621	ggtttccatattctcttccaagaatggaagtaataaataattttggaatgttaaaaaaaaaa	1680
QY	1681	aaaaa 1685	
Db	1681	aaaaa 1685	
RESULT 3			
AAC58588			
ID	AAC58588 standard; cDNA; 1685 BP.		
XX			
AC	AAC58588;		
XX			
DT	29-JAN-2001 (first entry)		
XX			
DE	Human PRO273 protein UNQ240 encoding cDNA SEQ ID NO:45.		
XX			
KM	Human: immune related disease; diagnosis; antiinflammatory; cardiant;		
KM	dermatological; antiarthritic; antrihematic; immunosuppressive;		
KM	haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;		
KM	antianeastic; hepatotropic; viroide; antiposortial; antiallergic;		
KM	antiallathmatic; systemic lupus erythematous; rheumatoid arthritis;		
KM	osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;		
KM	idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;		
KM	systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;		
KM	autoimmune thrombocytopaenia; immune-mediated renal disease;		

AA208965	AA208965 standard; cDNA; 1458 BP.
ID	AA208965 standard; cDNA; 1458 BP.
XX	
AC	AA208965;
XX	
DT	20-OCT-1999 (first entry)
XX	
DE	Macaque neokine-1 partial cDNA.
XX	
KW	Chemottractant cytokine; chemokine; CXC motif; conserved cysteine;
KW	signal transduction modulation; angiogenesis inhibition;
KW	chemotraction inhibition; cancer; inflammation; psoriasis;
KW	post-transplantation organ rejection; ds.
XX	
OS	Macaque sp.
XX	
EH	Key
FT	Location/Qualifiers
FT	3..284
FT	/*tag- a
FT	/partial
FT	/product= "Macaque neokine-1"
FT	/note="No start codon given"
FT	285..1458
FT	/*tag- b
XX	
PN	W09940104-A1.
XX	
PD	12-AUG-1999.
XX	
XX	10-FEB-1999; 99MO-US02943.
XX	
PR	10-FEB-1998; 98US-0023664.
XX	
PA	(MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
PI	Barnes TM, Mackay C;
XX	
DR	WPI; 1999-494271/41.
XX	
XX	P-PSDB; AAY31615.
XX	
PT	Novel neokine polypeptides and polynucleotides used for regulating
PT	and treating proliferative disorders and diseases
XX	
PS	Claim 1; Fig 4; 123pp; English.
XX	
CC	This sequence represents macaque neokine-1 cDNA. The neokines
CC	are a novel family of chemottractant cytokines (chemokines)
CC	and are ligands for a previously identified putative G
CC	protein-coupled receptor termed RDC1 (also called the neokine
CC	receptor). The neokines are members of the non-EUR-CXC
CC	subfamily of chemokines characterised by the absence of an
CC	EUR motif and the presence of a CXC signature motif. The CXC motif
CC	encompasses 4 highly conserved cysteine residues, with the first two
CC	cysteines separated by one non-conserved amino acid residue; however,
CC	the neokines show some atypical features which distinguish them from
CC	previously characterised CXC chemokines e.g., the presence of
CC	approximately 5 residues between the third and fourth conserved
CC	cysteines. The neokines have a variety of functions, including
CC	modulation of signal transduction, inhibition of angiogenesis,
CC	regulation of inflammation and inhibition of chemotraction.
CC	Neokines may therefore be useful in the treatment of various
CC	proliferative disorders or diseases: several types of cancer,
CC	inflammation, psoriasis, and immune rejection following skin graft
CC	and kidney transplantation. Neokines, their associated polynucleotides
CC	homologues and antibodies can be used in screening for drugs or
CC	compounds which modulate their activity and therefore may be important
CC	for the development of new therapeutics.
XX	
Sequence	1458 BP; 430 A; 350 C; 310 G; 368 T; 0 other;

Query Match	80.6%;	Score 1358.4;	DB 20;	Length 1458,
Best Local Similarity	96.1%;	Pred. No. 2e-271;		

[illegible]

QY 1296 gaaaacttaaaatataatgatgacatgacagctacagacacacatctgtg 1335
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 Db 1055 gaaaacttaaaatataatgatgacatgacagctacagacacatctgtg 1114
 QY 1356 acaagggaacaccttaaaagcgtgttcttcccccacacaaagacatgcaacta 1415
 |||||
 Db 1115 acaagggaacaccttaaaagcgtgttcttcccccacacaaagacatgcaacta 1174
 QY 1416 aagcaatattgtgtatcccatgtaattcttcaatgtaaacagtgcaactctt 1475
 |||||
 Db 1175 aagcaatattgtgtatcccatgtaattcttcaatgtaaacagtgcaactctt 1234
 QY 1476 cgaagcgaatagatgacatgacgcttcttccctgtacataatacccttaagaagccct 1535
 |||||
 Db 1235 caaaagcgaatagatgacatgacgcttcttccctgtacataatacccttaagaagccct 1294
 QY 1536 ccaacacatgccccagatataatgacgctgtactgctgtttatgtctatgacatg 1595
 |||||
 Db 1295 ccaacacatgccccagatataatgacgctgtactgctgtttatgtctatgacatg 1354
 QY 1596 tcagaaacattagcatgcatgcaagtttcataatcttcttaagaatggaataataa 1655
 |||||
 Db 1355 tcagaaacattagcatgcatgcaagtttcataatcttcttaagaatggaataataa 1414
 QY 1656 atatttgaatgtataaaaaa 1685
 |||||
 Db 1415 atatttgaatgtataaaaaa 1444

RESULT 7

ID AAZ42039 standard; cDNA: 1630 BP.

AC AAZ42039;

DT 31-JAN-2000 (first entry)

DE Human endometrium tumour cDNA derived EST 59.

KW Endometrium; human; tumour; cancer; anticancer; cytostatic; EST; treatment; uterine; gene therapy; expressed sequence tag; ss.

OS Homo sapiens.

PN DE19817948-A1.

PD 21-OCT-1999.

PF 17-APR-1998; 98DE-1017948.

PR 17-APR-1998; 98DE-1017948.

PA (META-) METAGEN GES GENOMFORSCHUNG MBH.

PI Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;

DR WPI; 1999-591957/51.

DR P-PSDB; AAY60116, AAY60117, AAY60118.

PT New nucleic acid sequences expressed in uterine cancer tissues, and derived polypeptides, for treatment of uterine and endometrial cancer and identification of therapeutic agents

PS Claim 3; Page 211; 444pp; German.

XX This invention describes novel human nucleic acid (cDNA) sequences (A), CC that are highly expressed in uterine tumour tissue and which have CC anticancer and cytostatic activity. (A) are used (i) for recombinant CC expression of polypeptides (B) and (ii) to isolate complete genes. (B) CC are used (i) to identify agents suitable for treatment of uterine or CC endometrial cancer; (ii) directly for treating these forms of cancer CC (including expression from gene therapy vectors) and (iii) for

CC generation of specific antibodies. (A) are identified by assembling ESTs CC (expressed sequence tags) from a particular tissue type before comparison CC of expression patterns. This allows a significantly longer fragment of CC the gene to be revealed, so should reduce the number of failures CC associated with the fact that ESTs from different libraries may represent CC different parts of the same unknown gene, distorting the estimated CC frequency of occurrence in a particular tissue. AAZ41981-742121 represent CC EST fragments derived from a human endometrium tumour cDNA library which CC encode the protein sequences represented in AAY59941-Y60328.

XX Sequence 1630 BP; 477 A; 392 C; 327 G; 434 T; 0 other;

Query Match 64.8%; Score 1092.2; DB 20; Length 1630;
 Best Local Similarity 99.7%; Pred. No. 1.9e-216;
 Matches 1094; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 575 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaagccttcttccacagcat 634
 |||||
 Db 532 acaaatataaaaaaaaaaaaaaaaaaaaaaaaaaaagccttcttccacagcat 591
 QY 635 aagacaaatataatattgtatgaagcacttttccaaagctgcaatttaccattt 694
 |||||
 Db 592 aagacaaatataatattgtatgaagcacttttccaaagctgcaatttaccattt 651
 QY 695 atagctgtgcgaagagctccagatggagaccatctctctgtcccaacttca 754
 |||||
 Db 652 atagctgtgcgaagagctccagatggagaccatctctctgtcccaacttca 711
 QY 755 tcacagctgtctttatcaaaaagggaactcaatgcttcttctttaaataatgct 814
 |||||
 Db 712 tcacagctgtctttatcaaaaagggaactcaatgcttcttctttaaataatgct 771
 QY 815 ttttgatattgtccatagcctacatcatccttagctttaaagccggagagaca 874
 |||||
 Db 772 ttttgatattgtccatagcctacatcatccttagctttaaagccggagagaca 831
 QY 875 atgaagctgtgacacatttcaatgtcagtgctccatctcagcttggaaagcttc 934
 |||||
 Db 832 atgaagctgtgacacatttcaatgtcagtgctccatctcagcttggaaagcttc 891
 QY 935 gcttagaagctcctgagcctcggacagctgcacagggctctctctgtggtatg 994
 |||||
 Db 892 gcttagaagctcctgagcctcggacagctgcacagggctctctctgtggtatg 951
 QY 995 ccaagcctcagtgtagcctccacagtgccctgtagccggcgaagcagagctctc 1054
 |||||
 Db 952 ccaagcctcagtgtagcctccacagtgccctgtagccggcgaagcagagctctc 1011
 QY 1055 ctgcatctgtctcctgaggaactcaagtttggtgcccagaaaatgtgtcattcccc 1114
 |||||
 Db 1012 ctgcatctgtctcctgaggaactcaagtttggtgcccagaaaatgtgtcattcccc 1071
 QY 1115 ctggttaattttacacacccctaggaacatttccaaatctgtgagtggaacaat 1174
 |||||
 Db 1072 ctggttaattttacacacccctaggaacatttccaaatctgtgagtggaacaat 1131
 QY 1175 gatccttaagaaggtgtgggtgttcccaacctgagagatttctgaaggttcaaggt 1234
 |||||
 Db 1132 gatccttaagaaggtgtgggtgttcccaacctgagagatttctgaaggttcaaggt 1191
 QY 1235 tcaatatttaattgtcgaagcagcagtggttcccaactgtcagaacacatttag 1294
 |||||
 Db 1192 tcaatatttaattgtcgaagcagcagtggttcccaactgtcagaacacatttag 1251
 QY 1295 agaaacttaaaatataatgatgacatgacagctacagacacacatctgtt 1354
 |||||
 Db 1252 agaaacttaaaatataatgatgacatgacagctacagacacacatctgtt 1311
 QY 1355 gacaaaggaaacaccttaaaagcgtgttcttccctcacaacagacacatgcaact 1414
 |||||
 Db 1312 gacaaaggaaacaccttaaaagcgtgttcttccctcacaacagacacatgcaact 1371

[illegible]

Db	635	acc-agggacgatttttaccatttatagctgctgctgaagagcttccagctgctgagatcc	693
QY	731	adctctctgtgctccaaacttcatcaaggctgtctttt-----atcaaaa	777
Db	694	agctgcgcctgcgcacacagacttcatcaagctgtcttctgtgcggcgctgtgcggggg	753
QY	778	aggggaaacatcattccttcccttctttaaanaagcttttcttatcttccataagctc	837
Db	754	cggggggaccctcaagccttcttctttaaanaaggggttctgtattgttccataagctca	813
QY	838	ctatacatctagacttcttataagcgcccgggagagacaatagcttctgtgacacatttca	897
Db	814	ccacacatctagacttcttataagcgctgcggagagacaagctgagatgttctgagacgttca	873
QY	898	ttgcagctgttctccatcttccatcttctggaagcttccgctcttaagagcttccgtgcctcg	957
Db	874	caggcactctctgcctgcgcacagcttcttcaaaagcttccgctctcagaagacgtgcgcctctg	933
QY	958	cadgaactgcacagcgctctctctgtgactatagcgcggtacagacagctcaagtgtatccaca	1011
Db	934	tgcgactgcacacagcctctcctctgtgactttagctgtctcagagtttcaagctgtaaccact	993
QY	1018	gtgcgcctctagccgcggcagaagcagagcagctctctctgcacatctgtctctctgaagaat	1077
Db	994	gtgcgcctctgttcaggagcaattgtggagcagcttcccttcatcactctgtgcttagaagaat	1055
QY	1078	caagtttgttgccagaaaatgtgccttacttccccctggttaattttacaacctta	1137
Db	1054	c-aggctacttaccagaagagcttcatctcccaaccc-----accaccacc	1099
QY	1138	ggaaacatttccaaagactcctgtgactgacgcgagacaatagtacattcaagaagctgctggggt	1197
Db	1100	gcaccccagctcattcccccgttcaacgcagcaggaagtgtacttcccttaagaagctgtgcttct	1155
QY	1198	ctt-ctccaaacctgaagattctctgaaagcttccacaggttccaatatttaagtcttcaaga	1256
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QY	1385	-----aaccttcaaaagcattgttcttcttcccttccacacaacaagaacatgcagactaaga	1420
Db	1340	cccccctcccaaaagcttgttcttcttcccttccaccccaagaagaagct-----	1390
QY	1421	ataatattgtattcccaactgaattcccttcaatgtttaaacagctgcagcttcccttgcga	1480
Db	1391	-----cccctcagtgaaatagcaaacagcactgttcttctctgaattagat	1455
QY	1481	gctaaatgacatgcagctgcctt-----tccctgttacaatacccttaagaagcccc	1534
Db	1436	gttagagacgactcctgcgccttgcctctctctgttcatatgtccttcaagaccctccc	1495
QY	1535	-----tcccaacacttgcgcgcgcgcagatctgcgcgaatgtactgtgtgttatatgc	1585
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FT	CDS	212..508	
FT		/*tag= b	
FT		/product= "Murine neokine-1"	
FT	3 UTR	509..1656	
FT		/*tag= c	
XX			
PN	WO940104-A1.		
XX			
PD	12-AUG-1999.		
XX			
XX	10-FEB-1999.	99WO-US02943.	
PE			
XX	10-FEB-1998.	98US-0023664.	
PR			
XX			
EA	(MIL-) MILLENNIUM BIOTHERAPEUTICS INC.		
XX			
PI	Barnes TM, Mackay C;		
XX			
XX	WPI: 1999-494271/A1.		
DR	P-PSDB; AAI31613.		
XX			
XX			
PT	Novel neokine polypeptides and polynucleotides used for regulating		
PT	and treating proliferative disorders and diseases		
XX			
PS	Claim 1, Fig 2; 123pp; English.		

CC This sequence represents murine neokine-1 cDNA. The neokines
CC are a novel family of chemottractant cytokines (chemokines)
CC and are ligands for a previously identified putative G
CC protein-coupled receptor termed RCR1 (also called the neokine
CC receptor). The neokines are members of the non-ELR-CXC
CC subfamily of chemokines characterised by the absence of an
CC ELR motif and the presence of a CXC signature motif. The CXC motif
CC encompasses 4 highly conserved cysteine residues with the first two
CC cysteines separated by one non-conserved amino acid residue; however,
CC the neokines show some atypical features which distinguish them from
CC previously characterised CXC chemokines e.g., the presence of
CC approximately 5 residues between the third and fourth conserved
CC cysteines. The neokines have a variety of functions, including
CC modulation of signal transduction, inhibition of angiogenesis,
CC regulation of inflammation and inhibition of chemotraction.
CC Neokines may therefore be useful in the treatment of various
CC proliferative disorders or diseases: several types of cancer,
CC inflammation, psoriasis, and immune rejection following skin graft
CC and kidney transplantation. Neokines, their associated polynucleotides
CC homologues and antibodies can be used in screening for drugs or
CC compounds which modulate their activity and therefore may be important
CC for the development of new therapeutics.

[illegible]

This sequence represents rat neokine-1 partial cDNA. The neokines are a novel family of chemottractant cytokines (chemokines) and are ligands for a previously identified putative G protein-coupled receptor termed RDC1 (also called the neokine receptor). The neokines are members of the non-ELR-CXC subfamily of chemokines characterised by the absence of an ELR motif and the presence of a CXC signature motif. The CXC motif encompasses 4 highly conserved cysteine residues, with the first two cysteines separated by one non-conserved amino acid residue; however, the neokines show some atypical features which distinguish them from previously characterised CXC chemokines e.g., the presence of approximately 5 residues between the third and fourth conserved cysteines. The neokines have a variety of functions, including modulation of signal transduction, inhibition of angiogenesis, regulation of inflammation and inhibition of chemotactraction. Neokines may therefore be useful in the treatment of various proliferative disorders or diseases: several types of cancer, inflammation, psoriasis, and immune rejection following skin graft and kidney transplantation. Neokines, their associated polynucleotides, homologues and antibodies can be used in screening for drugs or compounds which modulate their activity and therefore may be important for the development of new therapeutics.

Sequence 1372 BP; 359 A; 355 C; 332 G; 319 T; 7 other:

Query Match 35.8%; Score 604; DB 20; Length 1372;
Best Local Similarity 70.8%; Pred. No. 1.2e-115;
Matches 1021; Conservative 5; Mismatches 315; Indels 101; Gaps 13;

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QY 326 ctggaatagaagccaagtaaccgcactcgagaggaagatggtatcaccaccaga 385
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QY 386 agcgttcacagtaaccgagtaaccgtaaccgtaaccgtaaccgtaaccgtaaccg 445
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QY 446 cgttcacagtaaccgtaaccgtaaccgtaaccgtaaccgtaaccgtaaccgtaaccg 505
DB 181 cgttcacagtaaccgtaaccgtaaccgtaaccgtaaccgtaaccgtaaccgtaaccg 240
QY 506 gaaacacacagaaggaagaaacacacacagcttggaagatggtcgaagacattgca 565
DB 241 ggaacacacagaaggaagaaacacacacagcttggaagatggtcgaagacattgca 300
QY 566 gatttaaaaaaaataaaaaaaataaaaaaaataaaaaaaataaaaaaaataaaaaaa 625
DB 301 gatt-----ataaaaaaaataaaaaaaataaaaaaaataaaaaaaataaaaaaa 327
QY 626 cacaagcacaagaacaataatataatgtatgaagcaacttttaccacagctcagtt 685
DB 328 cacaagcacaaga--acaataatataatgtatgtgaagcctctcttacc--aggtcagtt 384
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DB 505 ttctcttttaaaaaatgaggtttttgtattgtccatagcactatatactgagctt 564
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DB 565 ataaagcccgaggagaacatgagcttggtggaacacattcattgacgtgtgtccg 624

QY 915 tctactgttggaagcttccgcttaagagtcctgagcctcggcagacagctgccaaggtc 974
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QY 1391 caccacacagac 1450
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QY 1451 aatgtaacagtgagctcctctctcgaagacgaagacacacacacacacacacacacac 1510
DB 1129 -----caacacagcagagctcctcttctg--gagtgagatgacacacacacacacac 1182
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DB 1183 acatattcttcaagac 1242
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DB 1362 aa 1363

RESULT 15

ID AAF94062 standard; DNA; 599 BP.

AAF94062;

23-MAY-2001 (first entry)

Primer specific for DNA encoding secretory/membrane protein SEQ ID 496.

Human; secretory protein; membrane protein; vaccine; gene therapy;

rheumatoid arthritis; diabetes; PCR primer; ss.

Synthetic.

Wed Jan 30 09:48:19 2002

us-09-978-189-369.rng

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Db 311 agcgagctgaaagctggaatgaagcacaagtaaccacacgtcgaggaagatggtt 370
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RESULT 2

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US-08-825-556A-1
; Sequence 1, Application US/08825556A
; Patent No. 5910431

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GENERAL INFORMATION:

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; APPLICANT: NI, Jian
; APPLICANT: Gentz, Reiner L.
; APPLICANT: Su, Jeffrey Y.
; APPLICANT: Li, Haodong
; TITLE OF INVENTION: Chemokine Alpha 2
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-2934

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COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,556A
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 435

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PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 60/013,653
; FILING DATE: 19-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0850001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540

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INFORMATION FOR SEQ. ID NO: 1:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 461 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

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; US-08-825-556A-1

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Query Match 25.9%; Score 435.6; DB 2; Length 461;
Best Local Similarity 98.7%; Pred. No. 1.8e-89;
Matches 450; Conservative 0; Mismatches 4; Indels 2; Gaps 1;

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Qy 490 ctacgaagaatagggtgaaacacccacgaaggaaacacccacgaagctgtggagactgt 549
Db 366 CTACGAAGAATAGGGTGAAAAAAGCTCAGAAAGGAAAGCTCCAAACAGTTGGAGACTTG 425
Qy 550 tg--caagagacttgcagattaaacacacacacacacacacacacacacacacacac 583
Db 426 TGGCAAGGAACCTTGCAGATTAAACAAAAA 461

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RESULT 3

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US-09-188-930-38
; Sequence 38, Application US/09188930A
; Patent No. 6150502

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GENERAL INFORMATION:

```

; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murlison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ. ID NOS: 348

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; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew

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DY 269 tccaaatgcaagtgtctcccgaagaggacccaagatccgctacagcgactgaagaagctg 328
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Db 1 tccaaatgcaagtgtctcccgaagaggacccaagatccgctacagcgactgaagaagctg 60

QY 329 gaatgaagccaaagtaccgcactgagagagaagatgttatcatcaccaccaagc 388
 Db 61 gaatgaagccaaagtaccgcactgagagagaagatgttatcatcaccaccaagc 120
 QY 389 gttccagagtcagagtcagagtcagagtcagagtcagagtcagagtcagagtc 448
 Db 121 gttccagagtcagagtcagagtcagagtcagagtcagagtcagagtcagagtc 180
 QY 449 ttcatcaagtgttacaacgcttgaaacgagagcgaggtcttaagaataag 502
 Db 181 ttcatcaagtgttacaacgcttgaaacgagagcgaggtcttaagaataag 234

RESULT 6
 US-09-188-930-271
 Sequence 271, Application US/09188930A
 Patent No. 6150502

GENERAL INFORMATION:
 APPLICANT: Watson, James D.
 APPLICANT: Strachan, Lorna
 APPLICANT: Sleeman, Matthew
 APPLICANT: Onrust, Rene
 APPLICANT: Murison, James Greg
 TITLE OF INVENTION: Compositions Isolated From Skin Cells
 TITLE OF INVENTION: and Methods For Their Use
 FILE REFERENCE: 11000.1011c1
 CURRENT APPLICATION NUMBER: US/09/188.930A
 CURRENT FILING DATE: 1998-11-09
 NUMBER OF SEQ ID NOS: 348
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO: 271
 LENGTH: 234
 TYPE: DNA
 ORGANISM: Mouse
 US-09-188-930-271

Query Match 12.7%; Score 214.8; DB 3; Length 234;
 Best Local Similarity 94.9%; Pred. No. 8.1e-40;
 Matches 222; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 QY 269 tccaatgaagtgtctccggaaggaaccagaatccgtctacagcgatgaagaagctg 328
 Db 1 tccaatgaagtgtctccggaaggaaccagaatccgtctacagcgatgaagaagctg 60
 QY 329 gaatgaagccaaagtaccgcactgagagagaagatgttatcatcaccaccaagc 388
 Db 61 gaatgaagccaaagtaccgcactgagagagaagatgttatcatcaccaccaagc 120
 QY 389 gttccagagtcagagtcagagtcagagtcagagtcagagtcagagtcagagtc 448
 Db 121 gttccagagtcagagtcagagtcagagtcagagtcagagtcagagtcagagtc 180
 QY 449 ttcatcaagtgttacaacgcttgaaacgagagcgaggtcttaagaataag 502
 Db 181 ttcatcaagtgttacaacgcttgaaacgagagcgaggtcttaagaataag 234

RESULT 7
 US-08-232-463-14/c
 Sequence 14, Application US/08232463
 Patent No. 5670367
 GENERAL INFORMATION:
 APPLICANT: DORNER, F.
 APPLICANT: SCHEIFLINGER, F.
 APPLICANT: FALKNER, F. G.
 TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
 NUMBER OF SEQUENCES: 52
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 1800 Diagonal Road, Suite 500
 CITY: Alexandria
 STATE: VA

COUNTRY: USA
 ZIP: 22313-0299
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/232,463
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/935,313
 FILING DATE:
 APPLICATION NUMBER: EP 91 114 300.6
 FILING DATE: 26-AUG-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,768
 REFERENCE/DOCKET NUMBER: 30472/114 IMMU
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703)836-9300
 TELEFAX: (703)683-4109
 TELEX: 899149
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7218 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 CLONE: pTZgpt-Fls
 US-08-232-463-14

Query Match 4.2%; Score 70.6; DB 1; Length 7218;
 Best Local Similarity 8.9%; Pred. NO. 1e-06; Mismatches 180; Indels 0; Gaps 0;
 Matches 40; Conservative 231; Mismatches 180; Indels 0; Gaps 0;
 QY 262 ggaaggtccaaatgaagtgtctccggaaggaaccagaatccgtctacagcgatgaa 321
 Db 1420 RRR 1361
 QY 322 gaagctgaaatgaagccaaagtaccgcactgagagagaagatgttatcatcaccac 381
 Db 1360 RRR 1301
 QY 382 caagaagctgtccaggtacagagtcagagtcagagtcagagtcagagtcagagtc 441
 Db 1300 RRR 1241
 QY 442 caagcgtctcaatgaagtgttacaacgcttgaaacgagagcgaggtcttaagaata 501
 Db 1240 RRR 1181
 QY 502 ggtgtaaaactcagaagagaaactccaacaggtggagagctgtlcaagaact 561
 Db 1180 RRR 1121
 QY 562 tgcagattaaaaaataaaaaaataaaaaaataaaaaaataaaaaaataaaagcttct 621
 Db 1120 RRR 1061
 QY 622 ttctcagagcatalaagacacaaatataatgttataagaagcattttaccaggtca 681
 Db 1060 AGCTCCCTCGACTGACCAAGCTCGGAATTATTCGTGTGAGGTATGCAACGAAG 1001
 QY 682 gtttacaatttaagctgtcggaag 712
 Db 1000 AAAATAGTTATAGTACCGCATCTGATGG 970

RESULT 8

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US-09-007-005-17
; Sequence 17, Application US/09007005B
; Patent No. 6258558
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihc
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; FILE REFERENCE: 00786/350003
; CURRENT APPLICATION NUMBER: US/09/007,005B
; EARLIER FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 289
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
; NAME/KEY: misc_feature
; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C or G
US-09-007-005-17

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Query Match          3.3%: Score 55.2; DB 4; Length 289;
Best Local Similarity 13.7%: Pred. No. 0.00081;
Matches 36; Conservative 101; Mismatches 125; Indels 0; Gaps 0;

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QY 340 aagtaaccgactgcgagagaagatgtatcatcaccccaagagcggtccagta 399
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 26 arururarcrarurururarcrarurgrnrrnrrnrrnrrnrrnrrnrrnrr 85
QY 400 ccgaggtcagagcactgcgcaccccaagctgcagacacgaagcgctcacaag 459
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 86 srrnrrsrrnrrsrrnrrsrrnrrsrrnrrsrrnrrsrrnrrsrrnrrsrrnrr 145
QY 460 gtacaacgcctgcagagcagcagcaggtctacaagaatagtgtaaacctcagaa 519
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 146 srrnrrsrrnrrsrrnrrsrrnrrsrrnrrsrrnrrsrrnrrsrrnrrsrrnrr 205
QY 520 gggaaacccaacacgctgggagactgtgcaagagacttgcagattaaaaaaa 579
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 206 srrnrrsrrnrrsrrnrrsrrnrrsrrnrrsrrnrrsrrnrrsrrnrrsrrnrr 265
QY 580 aaaaaaaaaaaaaaaaaaaaaa 601
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DB 266 aaaaaaaaaaaaaaaaaaaaaa 287

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RESULT 9
US-09-244-796-17
; Sequence 17, Application US/09244796
; Patent No. 6281344
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihc
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; FILE REFERENCE: 00786/350007
; CURRENT APPLICATION NUMBER: US/09/244,796
; EARLIER FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06

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; EARLIER APPLICATION NUMBER: 09/007,005
; EARLIER FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 289
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
; NAME/KEY: misc_feature
; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17

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Query Match          3.3%: Score 55.2; DB 4; Length 289;
Best Local Similarity 13.7%: Pred. No. 0.00081;
Matches 36; Conservative 101; Mismatches 125; Indels 0; Gaps 0;

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      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 26 arururarcrarurururarcrarurgrnrrnrrnrrnrrnrrnrrnrrnrr 85
QY 400 ccgaggtcagagcactgcgcaccccaagctgcagacacgaagcgctcacaag 459
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DB 86 srrnrrsrrnrrsrrnrrsrrnrrsrrnrrsrrnrrsrrnrrsrrnrrsrrnrr 145
QY 460 gtacaacgcctgcagagcagcagcaggtctacaagaatagtgtaaacctcagaa 519
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DB 146 srrnrrsrrnrrsrrnrrsrrnrrsrrnrrsrrnrrsrrnrrsrrnrrsrrnrr 205
QY 520 gggaaacccaacacgctgggagactgtgcaagagacttgcagattaaaaaaa 579
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 206 srrnrrsrrnrrsrrnrrsrrnrrsrrnrrsrrnrrsrrnrrsrrnrrsrrnrr 265
QY 580 aaaaaaaaaaaaaaaaaaaaaa 601
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DB 266 aaaaaaaaaaaaaaaaaaaaaa 287

```

```

RESULT 10
US-08-378-313-24
; Sequence 24, Application US/08378313
; Patent No. 6207881
; GENERAL INFORMATION:
; APPLICANT: THEOLOGIS, ATHANASIOS
; APPLICANT: SATO, TAKAHIDO
; TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH
; TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/378,313
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/862,493
; FILING DATE: 02-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.

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QY 492 acgaagataggtgtaaaacctcagaaggaaaactccaaaccagtgtggaagactgtg 551
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Db 252 ACTAGGGCTAAGATGAGCCACCTTAAGAAGGAAAAATTAGAGTCAAGAAAAGAAAGGAAG 193

Patent No. 6096504	GENERAL INFORMATION:	
APPLICANT: MCGONIGLE, BRIAN	APPLICANT: O'KEEFE, DANIEL	
TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES	FILE REFERENCE: CL-1128-A	
CURRENT APPLICATION NUMBER: US/09/248,335	CURRENT FILING DATE: 1999-02-10	
EARLIER APPLICATION NUMBER: 08/924,759	EARLIER FILING DATE: 1997-September-05	
NUMBER OF SEQ ID NOS: 74	SOFTWARE: Microsoft Word Version 7.0A	
SEQ ID NO 25	LENGTH: 1279	
TYPE: DNA	ORGANISM: maize	
US-09-248-335-25		
Query Match:	3.2%; Score 53.4; DB: 3; Length 1279;	
Best Local Similarity	63.8%; Pred. No. 0.0038; Indels 0; Gaps 0;	
Matches 81; Conservative 0; Mismatches 46;		
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DB 1138 gttcgtcgtgtaataaatgaaaacccaccccgcttggatgaatcattcattcagtg 1197		
QY 547 ttgtcgaagagacttgcagatttaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 606		
DB 1198 tctgtgtaa 1257		
QY 607 aaaaaa 613		
DB 1258 aaaaaa 1264		
RESULT 15		
US-08-484-105-17		
Sequence 17, Application US/0844105		
Patent No. 5589341		
GENERAL INFORMATION:		
APPLICANT: STILLMAN, Bruce		
APPLICANT: BELL, Stephen P		
APPLICANT: KOBAYASHI, Ryuji		
APPLICANT: RINE, Jasper		
APPLICANT: FOSS, Margit		
APPLICANT: MCNALLY, Francis J		
APPLICANT: LAURENSEN, Patricia		
APPLICANT: HERSHKOWITZ, Ira		
APPLICANT: LI, Joachim J		
APPLICANT: GAVIN, Kimberly		
TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES		
NUMBER OF SEQUENCES: 24		
CORRESPONDENCE ADDRESSES:		
ADDRESSEE: FLEHR, HONBACH, TEST, ALBRITTON & HERBERT		
STREET: 4 Embarcadero Center, Suite 3400		
CITY: San Francisco		
STATE: California		
COUNTRY: USA		
ZIP: 94111-4187		
COMPUTER READABLE FORM:		
MEDIUM TYPE: Floppy disk		
COMPUTER: IBM PC compatible		
OPERATING SYSTEM: PC-DOS/MS-DOS		
SOFTWARE: PatentIn Release #1.0, Version #1.30		
CURRENT APPLICATION DATA:		
APPLICATION NUMBER: US/08/484,105		
FILING DATE:		
CLASSIFICATION: 435		
ATTORNEY/AGENT INFORMATION:		
NAME: Osman Ph.D., Richard Aron		
REGISTRATION NUMBER: 36,627		
REFERENCE DOCUMENT NUMBER: 50033		

Wed Jan 30 09:48:19 2002

us-09-978-189-369.rni

Page 8

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 3214 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 220..2802
US-08-484-105-17

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Best Local Similarity 75.9%; Pred. No. 0.0054;
Matches 66; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

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DB 3110 CTCCTCAGTGTGGGAGCTTTCATTAATTAATTCCTTTTAAAAA 3169
QY 587 AAAAAAAAAAAAAAAAAAAAAA 613
DB 3170 AAAAAAAAAAAAAAAAAAAAAA 3196

Search completed: January 30, 2002, 04:05:50
Job time: 6998 sec

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BASE COUNT 263 a 234 c 201 g 278 t
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Query Match 50.2%; Score 846.4; DB 11; Length 976;
Best Local Similarity 97.7%; Pred. No. 1.3e-110;
Matches 891; Conservative 0; Mismatches 16; Indels 5; Gaps 3;

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Db 181 TTCTCTTTTAAAAATGCTTTTGTATTTGTCCATGCTCATATACATCTGAGCTTTA 240
Qy 856 taagcgcgggaggaagaatagcttgtagacacattcaltgcaagtgtgtccat 915
Db 241 TAAAGCCCGGAGAGACATAGCTTGATGAGACATTTATGACATGCTGCTCAT 300
Qy 916 cctaagcttgggaagcttcgcttagagtcctgctgctgctgctgctgctgctgct 975
Db 301 CCTAGCTTGGGAAGCTTCCGCTTGAAGGCTGCGCGCCGCGCACAGCTGCCACGGGCTC 360
Qy 976 tcttgagctatggcgcgtagacagctagtgtagctcacaagtgcccttgaacgg 1035
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Qy 1036 caagcggagcagctcctctgcatctgtctctgaggaactcaagtttggtccagaa 1095
Db 421 CAAGCAGGAGCAAGTCTCTGCACTCTGCTGAGCACTCAAGTTGTTGCCAGAA 480
Qy 1096 aaatgtgtcattcccccctggttaatttttaacacacctgagaaacatttccaaagtc 1155
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Qy 1156 ctgttgtagcagaaagaaatgctttaaagaaagtggtggtccttccaaactgaagat 1215
Db 541 CTGTGATGGGAGACAAATGATCTTAAAGAAAGGTGGGCTTTCCCAACCTGAGAT 600
Qy 1216 ttctgaaggttcacaggttcaatatttaagtcttcaagaagatgtaggttccaaac 1275
Db 601 TTCTGAAGGTTACAGGTTCAATATTATGCTTCAAGACATGAGGTTCCCAACAC 660
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Qy 1336 taagaacacacattcgttgaagaagaaacctcaagaatglttcttccctaaca 1395
Db 721 TACAGACACACATTTGTTGACAAAGGAAACCTTCAAAAGCATGTTCTTCCCTCA -CA 779
Qy 1396 caacagaacatgcaactaagaacatataatgttattcccaatgtaacttccaaagt 1455
Db 780 TAAACAGAAATGCACTAAAGCAATATATGATTTCCCATTAATTTCTTCAACAG 839
Qy 1456 taacaagtg---cagctccttctcg-aagctaaagtagccatggcccttccctctcga 1511
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Db 900 CATATTACCTTA 911

RESULT 2
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LOCUS 602659321F1 NCI-CGAP_Skin3 Homo sapiens cDNA clone IMAGE:4802404 5',
DEFINITION mRNA sequence.

ACCESSION Bg696197
VERSION Bg696197.1 GI:13961096
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 858)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps@email.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLNL0696 row: j column: 05
High quality sequence stop: 852.
Location/Qualifiers

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/clone_1lb="NCI-CGAP_Skin3"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: PCMV-SPORT6; Site: 1: NotI; Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI-CGAP Library."

BASE COUNT 228 a 211 c 176 g 243 t
ORIGIN

Query Match 49.6%; Score 835; DB 11; Length 858;
Best Local Similarity 99.8%; Pred. No. 5.6e-109;
Matches 857; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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Qy 722 gggagaccatctctctgtgctccagaactcaacagctgctttttcaaaaagg 781
Db 61 GGGAGACCAATCTCTGTGCTCCAGACTTCAACAGAGCTGCTTTTATCAAAAAGG 120
Qy 782 gaaactaagcttcttctttaaanaagcttttggtaattgtgtccatagctacat 841
Db 121 GAAAACTATGCTCTTCTTTTAAAAAATGCTTTTGTGATTTGTCATACATGCTAT 180
Qy 842 acatctgagcttataagcgcgggaggaacaatgagctgtgtgacaacattcattgc 901
Db 181 ACATGTAGCTTTTAAAGCGCCGCGAGAGAACATGAGCTTGTGGACACATTTCAATTGC 240
Qy 902 agtgtgtcattctctcagcttgggaagcttcgcttagaaggtctctggcctggaca 961
Db 241 AGTGTGTCTCAATCTCTGAGCTTGGGAACCTTCCGTTAAGAGTCTCGGCTCTGGCACA 300
Qy 962 gctgcacaggtctctccgggcttataggcggtagacagctcagtgtaactcacaagtg 1021
Db 301 GCTGCCACGGGCTCTCTGCGCTTATGGCCGCTACACACCTCACTGAGTGCACAGTGG 360

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/db_xref="taxon:9606"  
/clone="IMAGE:4750167"  
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Best Local Similarity	99.6%;	Pred. No. 8.6e-105;		
Matches 826;	Conservative	0;	Mismatches 1;	Indels 2;
				Gaps 2

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OY	714	ttccagaatgggaagaccatctctcttgtagtccaaacttcaacaagctctgctttatc	773
Db	61	tttccAATGGGAGAGACCCAtCTCTCTTtGGtCTtCAAGAtTTCAtCAAGGcttGCTTTTATtC	120
OY	774	aaagaagggaagaactcaatgaccttccctttttaaanaatgcttlttltgatttgcac	833
Db	121	AAABAGGGAAGAACTCAATGcCTTTCCTTTTAAAAAAGCTTTTGTATTTGTCATAC	180
OY	834	gttcacatcatctgtagctttaaagcccgaggagaaatagacttgtagaacat	893
Db	181	gttCACTATCACTGAGCTTATATAGCCCGGAGAGAAATAGCTTGtGTGAGACAT	240
OY	894	ttcatttgaaagtgtgtcccatctctaagcttgggaagcttccgcttaagatctctgagcc	953
Db	241	tttCAATTGcAGtGTtGCTtCCATCTCCATGGCTTGGAAAGCTTCGGTtTAGAGtTCtGGCGCC	300
OY	954	tctgacagacttgcacagggactctctgagctttaggcctgtagccggttcaagctcaagtgtgactc	1011
Db	301	tctGcACAGcttGtCCACGGGctCTCCTtGGcCTTATtGGCGGtCAAGcCTCAgTGTGATC	360
OY	1014	caacgttgccccctgttagccgggcaagcagagcagagctctctgcactgttccctgaag	107
Db	361	CACAGTGGCCCCtGTtAGCGGGGAGCAAGAGAGAGAGtCTCTtGtCACTtTtCTtCGAGG	420
OY	1074	aactcaagtttggtgtgcagaaaaatgtgctcatctcccccgtgttaatttttacacac	1133
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OY	1194	gggtcttttcccaaacctgagatcttctgaaagttcacaggtttcaatatataagcttga	125
Db	541	GGGCTTtCCCAACtGAGAtTtTCTtAAAGtTtCACAGStTtCAATtTtTtTtAAgtCTtCAG	600
OY	1254	aagdatgtgaagtttcccaacactgtcagcaaaaaacttaagagaaaaacttaaaatata	131
Db	601	AAGATGTGAGGtTtCCCAACAtCTGTcAGCAAAAAAActTAGGAAGAAAACTTAAAAATATAT	660
OY	1314	gaatacatagcgcaataacagacttacaagaaacacacttctgttgcagaaggaaaaacttcaa	137
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OY	1374	agcatgttcttcttccctcaccaacacagaaacatgcagtaacaaagatatatttggat	143
Db	721	AGCAgtTtTtTtTtTtTtTtCCtCAACA - AACAGACAtTtGCAAGTACTAAAGCAATATtTtGTAT	779
OY	1434	tctccatgtaattcttcaatgtaaacagtgagctctcttcttogaagcta	1484
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LOCUS	602627337FI NCI.CGAP.Skn4 Homo sapiens cDNA clone IMAGE:4752104 5'	844 bp	mRNA
LOCUS	602627337FI NCI.CGAP.Skn4 Homo sapiens cDNA clone IMAGE:4752104 5'	844 bp	mRNA

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 VERSION BG679254.1 GI:13910651
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 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 844)
 NIH-MGC http://mgs.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@biml.nih.gov
 Tissue Procurement: James Cleaver, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at: http://image.llnl.gov
 Plate: LLM10609 row: j column: 09
 High quality sequence stop: 839.
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 QY 771 atcaaaagggaactcagctctctctttaaataatgcttttcttcttca 830
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 QY 1011 ctccacagtgccctctgtaacgggacagagagcgagctctctgcatctctctc 1070
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 QY 1071 aggaaccagagtggtgtgcagaaatgtgtctcattcccccctgtaattttaca 1130
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 QY 1251 cagaagcatggtggttcccaaccgagagattctgaaaggttcaaggttcaattattatgctt 1310
 DB 541 CAGAGCATGTGAGGTTTCCCAACCTGAGGATTTGTGAAGGTTTCACAGGTTCAATATTATGCTT 600
 QY 1311 tatgaatcacatgagcaatcacagctacagcaacacatctgttgcagggaaacacct 1370
 DB 601 TATGAATACATGGCGAATACAGCTACAGCAACACATCTGTGTGACAGGGAACCTT 660
 QY 1371 caaagatgttcttccctccaccacaagaaacagcagctacagctacagcaatatttgc 1430
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 DB 721 GATTCGCCCATGTAATTTCTCAATGTTAAACAGTGCAATCTCTTGCAGAAAGCTAAGATGA 780
 QY 1491 ccattgagccttctctctgtacataacaccttaagaagccctccacaactgcccc 1550
 DB 781 -CATGCCCTCTTCTCTGTACATAT-TCCTTAAGAACGCCCTCCACACA--TGACCC 835
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 DEFINITION prime, mRNA sequence.
 AL543855
 AL543855.1 GI:12876334
 VERSION
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 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 845)
 Li, W.-B., Gruber, C., Jessee, J., and Polayes, D.
 Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 Location/Qualifiers
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 /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifestech.com url : http://fulllength.invitrogen.com"
 BASE COUNT 231 a 204 c 166 g 227 t 17 others
 ORIGIN
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Best Local Similarity 97.3%; Pred. No. 1,le-103;									
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Oy	958	cacagctgcacagggctct-cctgggttatgcccgttcaagcctcaat-gtgaactca	1015						
Db	241	CACAGCTGCACGGGCTCTTACCTGGCTTATGGCGGTCACAGCTTCATGACTCCA	300						
Oy	1016	cagtgagccctgtagccgggcaagcagagagagctctctgactgtctctgagaa	1075						
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SOURCE human.									

ORGANISM Homo sapiens									
REFERENCE 1 (bases 1 to 794)									
AUTHORS NIH-MGC									
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)									
JOURNAL Unpublished (1999)									
COMMENT Contact: Robert Strausberg, Ph.D.									
Email: cgabbs-remail.nih.gov									
Tissue Procurement: James Cleaver, M.D.									
DNA Library Preparation: Life Technologies, Inc.									
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)									
DNA sequencing by: Incyte Genomics, Inc.									
Clone distribution: MGC clone distribution information can be									
found through the I.M.A.G.E. Consortium/LLNL at:									
http://image.llnl.gov									
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Technologies. Note: this is a NCI_CGAP Library."									
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210 a 191 c 167 g 226 t									
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Db	181	GTCACTATACATCTGAGCTTTATAGCGCCCGGAGAGCAATGAGCTTGTGACAT	240						
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 VERSION BG679890.1 GI:13911287
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 SOURCE human.
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 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 860)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: rgs@bbs-rcmail.nih.gov
 Tissue Procurement: James Cleaver, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: L1AM10607 row: 1 column: 24
 High quality sequence stop: 858.
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 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 817)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgsb@r-email.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LCM1331 row: a column: 01
 High quality sequence stop: 805.
 Location/Qualifiers

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 C, or G and N = A, C, G, or T). Average insert size 1.65
 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
 by PCR. This library was enriched for full-length clones
 and was constructed by Clontech Laboratories (Palo Alto,
 CA). Note: this is a NIH_MGC library."
 BASE COUNT 220 a 202 c 170 g 225 t
 ORIGIN

Query Match 42.4%; Score 714.6; DB 11; Length 817;
 Best Local Similarity 98.4%; Pred. No. 5.7e-92;
 Matches 796; Conservative 0; Mismatches 4; Indels 9; Gaps 7;
 Db 844 atctagcttlaaagccgagaggaacatgagcttgtagacatcttcaatgag 903
 1 ATCTGAGCTTATAGCCGCCCGGAGGAAACATAGCTTGGTGACACATTTCATTCAG 60
 Oy 904 tttgtctcaatctagcttgaggaaagcttcgcttagagcttcgagccttcgacagc 963
 61 TGTGTCTCCATTCTCAGCTTGGGAAAGCTTCGCTTAGAGTCTCGGCGCTCGGACACGC 120
 Oy 964 tgcacagagctctctgagcttagagccggtcaagctcagctgagctcagctgagc 1023
 121 TGCCAGGGGCTCTCTGGGCTTATGGCGGTACAGCCTCAGTGTGACTCCACAGTGGCC 180
 Oy 1024 cctttagcgggcaagcagagcagctcctcgtcagctcagctcagctcagctgagc 1083
 181 CCTGAGCCGGGCAAGCAGGAGGAGTCTCTGTCATCTGTTCTGAGGAACTCAAGTT 240
 Oy 1084 tgggtgcagaaaatgtgtctcattcccccgtgttaattttacacacccctagaaac 1143
 241 TGGTGGCCAGAAAATGCTTCATTCCTCCCTGTTAAATTTTACACACCTTAGGAAC 300
 Oy 1144 attccaagatccgtgagcagagacaatgacccctaaagaagtggtggtcttcc 1203
 301 ATTTCGAAGATCTGTGATGCGGACAAATGATCTTAAAGAGGTGGGGCTTTTC 360
 Oy 1204 caaccgaggaatttcgaaaggttcaagttcaatlaattatgctcagaagcatgta 1263
 361 CAACCTGAGATTTCTGAAGGTTACAGGTTCAATATTTAAAGCTTCACAGCATGTGA 420
 Oy 1264 ggttcccaaacgttcgagaaaacctaagagaaaacctaataatagatgacatgc 1323
 421 GGTTCCTCAACACATCTGACGCAAAAACCTTAGAGAAAACCTTAAATATGATATACATGC 480
 Oy 1324 gcaatcacagcttacaagacacattctgtgcaagagaaaacctaataatgacatgctc 1383
 481 GCAATCACAGCTACAGACACATTTCTGTGACAAAGGAAACCTTCAAGCATGTTTC 540
 Oy 1384 ttccctcacacaagaagaacatgagctactaaagaacataatt-tgtatctcccatgt 1442

Db 541 TTTCCTCACACAGACAGACATGCACTAAGCAATATATCTGTGATCCCAATGT 600
 Oy 1443 aatt--cttcaatgttaaacagctgagctcctcttcgaaagctagatgacatgagc 1500
 601 AATTCTCTTCAATATGTTAAACAGTGCAGTCTTTCGAAAGCTAAGATGACATGCGCC 660
 Oy 1501 ttctctctgt-acatatacccttaagaagcccccctcacacactgcccccatatag 1559
 661 TTTCCTCTGTAACATATACCTTAAAGAGCCCTCCACA-ACAGCCCCCATTAATAG 719
 Oy 1560 ccgc-attgtaactgctgtatatagtcatatgacat-gtcagaacatlaagcatgcat 1617
 720 CCGCATGTGATGTCG--TGTATATGCTATGATACATGCTAGAAACATTAATGATCTT 777
 Oy 1618 gcaggttcaatcttcttcaatagatgaa 1646
 778 GCAGGTTCAATATCTTCTTAAGATGAA 806

RESULT 9
 AL570175/c
 LOCUS
 DEFINITION AL570175 LTI_NFL006.PL2 Homo sapiens cDNA clone CSDDI005122 3
 prime, mRNA sequence.
 ACCESSION AL570175
 VERSION AL570175.1 GI:12926227
 KEYWORDS EST.
 SOURCE human.
 ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 745)
 L.H.W.B., Gruber,C., Jesse,J. and Polyes,D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
 source
 location/Qualifiers
 1. 745
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CSDDI005122"
 /clone_lib="LTI_NFL006.PL2"
 /tissue_type="placenta"

/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed by
 Life Technologies. Contact: Feng Liang Life Technologies,
 a division of Invitrogen 9800 Medical Center Drive
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@life.com
 http://fulllength.invitrogen.com"

BASE COUNT 200 a 150 c 179 g 205 t 11 others
 ORIGIN
 Query Match 41.3%; Score 696.6; DB 10; Length 745;
 Best Local Similarity 97.4%; Pred. No. 2e-89;
 Matches 726; Conservative 11; Mismatches 9; Indels 3; Gaps 3;

Oy 792 gcccttccttlaaanaatgcttttttttttttttttttttttttttttttttttttttt 851
 Db 745 RCCTTCTCTTTTAAATAATGCTTTTGTATTTGTCATGCTACTATATATCTGAGC 686
 Oy 852 ttataaagcccgagaggaacatgagcttgtagaacatcttcaatgacatgctc 911
 685 TTTATAGCGCCCGGAGGAGCAATGAGCTTGTGACACATTTCAATGCAATGTTGCTC 626

T.T. 08c 20

560 ttgcagattaaaaaaaaaaaaaaaaaaaaaaaaaaagcctt 619

Db 580 TTTCAGATT-----AAAATAAAAGCCCTTT 605

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Qy 620 cttctcagcgaataagacacaaatataatgttatgaagcattttacacagct 679
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Db 606 cttctcagcgaataagacacaaatataatgttatgaagcattttacacagct 662
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 680 cagttttacatttatatgctgctgagaaagcttcacagtggaacacatctctt 739
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 663 GAGTATTACATTTATATAGCTGTGTGTAAGAGCTTCACAGATGTAGTCCAGCTCCCT 722
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 740 gtgtccagactcaccagctgcttllt-----atcaaaaggaggaaa 786
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 723 GCGCACGACACTCTATACAGTGGCTTTTGTGGCGGCTTGGCGGGGGGAG 782
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 787 ctcatgcttcttctttaaataatgtctttttatlt-gtccatagctatcat 845
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 783 CTCAGCCTTTCTTTTAAATAGGGGTTTGTATTTGGTCCATATGTACACACAT 842
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 846 ctgagcttataagcgccggaggaaacagagctgtgtgacacatttcaatgca 905
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Db 843 CTGACCTTTATTAACGCTGGGAGACACATGA-CATGTTAAGCGGTTCCAGCATA 901
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 906 ttgtccatctcctatgtagaagcttcogcttagaggtccctgagcctcgacagctg 965
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 902 CT-CTCCGCTCCAGCTTAACAAGCTCCGCTCAGAGACATGGGGCTCTGCGCAGCTG 960
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 966 -ccaagggctctcctgggtatagcggtacagcctcaagtgtgactccaagtg-cc 1023
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 961 CCCACAGGCTCTCTGGGCTTATGACTGTCAGACTTTTCAGTGACTCCACTGTGGCC 1020
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1024 cctgtagcgggcaagcagcagcagctctctctgcatctgtctctgagaaatca 1083
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1021 CCTGTTCAGAGGCAATGGGAGACAGGCTCTTACATCTGTGCTTACAGAGACTC-AGTC 1079
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1084 tgggttcagaaatgtgtctcatctccctgtgttaattttacacaccttagaaac 1143
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1080 TACTTACCAAGAGACTTATCATCCACCC-----ACCCACCCGACCC 1126
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1144 attccaagatctgtgtagcagacaaatgatcccttaagaagtggtgtctt-ct 1202
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1127 CAGCTATTCCCTGTGACAGCAGGCAAGTATCTTAAAGAGCTGGGTCTTTTCTT 1186
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1203 ccaacctggaatcttgaaaggttcacaggtcacaatataatgttcagaagatgtg 1262
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1187 GCNAATGTAGGGTTTGTGAAGGTCCCTGTGTGTGAAGATGCTCTGAGCATCCA 1246
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Qy 1263 aggttcccaactgtcagcaaa-----aaccttagggaaacttaaatat 1313
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1247 AAGTCCCAAGCACTGTGAAGAAATGATGCTCGATGTTCCGGAGGACAAAGCATGCG 1306
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Qy 1314 gaatacatgcaatacacagctacacacatctgttgaagaaggaa-----aa 1366
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1307 GATTAGATGACAGACACACAGCCAGCATACATCTCTGGCATGGAGCTCCCC 1366
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1367 ccttcaagaatgttcttccctcaacacagaacatgcaagtactaagaatata 1426
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1367 CCCCAGAGCTTTGTCTTCTCCCTCACCCACACAGAAAGGCACT----- 1411
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1427 ttgtgtatcccatgttaattcttcaatgtttaaagctgagctcttcttgaaga 1486
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1412 -----CCCTCTGTAATAACCAACACAGCACTGTTCTGTGATTAGATGTTAG 1462
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Qy 1487 atgacatgagccttctcct-----tgtacataacccttaagaagcgcgc----- 1534
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1463 ACGATCTGGGCGCTCTCTCTCTGTGTATATATGCTTACAGTACCCCTCCACGCC 1522
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Qy 1535 ----tccaacactgccccagatatatgctgactgtgtgttataatgtctatgta 1591
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Db 1523 CATGCCACACACTGCCCTCTATTAGAGCGCAGCTGTATGGCTGTG-TACTGCTATGTA 1581
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Qy 1592 catgtcagaacattatgcatgtcatgttcatatctcttcaagaatg-----ga 1645
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Db 1582 AATGCTGAGACCCCTGAGTGTGATGCAAGTTTCATGTTCTTCTTATGATGAAGAGA 1641
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1646 aagtaataaataatattgaat 1668
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Db 1642 AAGTATTAATAATATTATTAAGT 1664
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RESULT 12
BG699665 770 bp mRNA EST 07-MAY-2001
602681510F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4814139 5',
mRNA sequence.
ACCESSION
BG699665
KEYWORDS
SOURCE
ORGANISM
human
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 770)
AUTHORS
NIH-MGC http://mgi.nci.nih.gov/
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: gcrabs-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shihaki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL0709 row: c column: 04
High quality sequence stop: 568.
location/Qualifiers
1..770
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4814139"
/clone_lib="NIH_MGC_95"
/tissue_type="hippocampus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescript (modified
pBluescript KS+); Site:1: BamHI; Site:2: SalI-XhoI (gtcag
5'-Oligo-dT primed using primer 5'-TTTTTTTTTTTGTG-3',
size-selected for average insert size 2.5 kb and
normalized to 10^5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT
191 a 243 c 214 g 122 t
ORIGIN
Query Match 37.9%; Score 638.6; DB 11; Length 770;
Best Local Similarity 92.5%; Pred. No. 3; le-81;
Matches 715; Conservative 0; Mismatches 29; Indels 29; Gaps 3;
Qy 4 gagaacagcagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 63
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4 GGGACAAAGCGAGACGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 63
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 64 agcggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 123
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 64 AGCCGAGCGACAGCAGAGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 123
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 124 tggcgtctccggcgccgcctccgagcgagcagcagcagcagcagcagcagcagcag 183
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 124 TGGGCTCTCCGGCGCGCGCTCCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 183
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 184 ccgcgcctccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 243
  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 184 CCGCGCGCTCCGCGATGAGGCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 243
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QY 244 gctgtacacgcgcgtgtgtgacgggtcccaatgtaagtgctcccggaagaccacgaat 303
 Db 244 GCTGTACACGCGCGTGTGTGACGGGTCCCAATGTAAGTGCTCCCGGAAGACCAACAT 303
 QY 304 ccgcttcaacgcgcgtgtgaaagctgtgaaatgtaagcccaagtaaccgcactgcgaagaa 363
 Db 304 CCCTTACACGCGCGTGTGAAAGCTGTGAAATGTAAGCCCAAGTACCCGCACTCGAGAGAA 363
 QY 364 gatgtatcatcaccacccaagagctgtccaggtaccaggtgagggacgtcccgca 423
 Db 364 GATGTTATCATCACCAACCAAGCGCTGTCCAGGTACCGAGTACAGGACACTCGCTGCA 423
 QY 424 ccccaagctgcagagacccaagcgtctcatcaagtgtgtacaagcgtgtgaaagaaq 483
 Db 424 CCCCAAGCTGCAGAGACCCACCAAGCGCTTCATCAAGGTGTACAAGCGCTGGAACGAAGCG 483
 QY 484 caggtgtcagagataggtgtgaaacccctcagaaggaagaaactccaacagttgga 543
 Db 484 CAGGTGTCAAGAAATAGGTTGAAACCTCAGAGGGAAGCAACCTCCAAACAGTTGGGA 543
 QY 544 gactgtgcaagagactgtgcagattaaacacacacacacacacacacacacacacac 603
 Db 544 GACTGTGCAAGACTTGTGAGATT-----ACCAACACAC 579
 QY 604 aaaaaaaagcgttcttctcagaagcacaagacacacacacacacacacacacacacac 660
 Db 580 CCAAAAAAGCGCTTCTTCTCAGGGCTTACAGACCAAAATTACTATATAGGTAATGA 639
 QY 661 agcacttttcaacagctcagttttacat--ctttagtggtgaggaagcttcca 718
 Db 640 AGCACTTTTTCACACGGTCTTCTCAGGCTTACATTCATTACGCTGCTTCCGACGCTTCCA 699
 QY 719 gatgggaacccatctctctgtgtcctcagactcaccacagctgtcttca 771
 Db 700 GATGGGAACCCATCTCTTGTGCTCCACAGACTTACACACGCGCTTCTTA 752

RESULT 13
 LOCUS BG572071 858 bp mRNA EST 10-APR-2001
 DEFINITION 60259254F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4719754 5',
 mRNA sequence.
 ACCESSION BG572071
 VERSION BG572071.1 GI:13579724
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 858)
 NIH-MGC <http://mgi.ncl.nih.gov/>
 National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: CLOUTTECH Laboratories, Inc.
 cDNA Library Preparation: CLOUTTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1CM1573 row: f column: 11
 High quality sequence stop: 635.
 Location/Qualifiers
 1. 858
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4719754"
 /clone_1ib="NIH_MGC_79"
 /lab_host="DH10B (TI phage-resistant)"
 /note="Organ: placenta; Vector: pNR-LIB (Clontech);
 Site_1: SfiI (ggccgctcgcc); Site_2: SfiI (ggcattatggcc

BASE COUNT

296 a 196 c 176 g 190 t

ORIGIN

Query Match 37.1%; Score 624.6; DB 11; Length 858;
 Best local similarity 98.5%; Pred. No. 2.8e-79;
 Matches 641; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 1036 caagcagagcagagctctcgtcgtcgtctctcgtgagaaactaagttgttgcagaa 1095
 Db 1 CAGCAGAGAGCAGGCTCTCTGCACTCTCTGAGAACTCAAGTTTGTTGCCAGAA 60
 QY 1096 aaatgtgtcattcccccctggttaatttacaacacctagaacacattccaagatc 1155
 Db 61 AAATGTGTTTCAATCCCGCTGGTTAATTTTACACACCCAGGAACATTTCCAGATC 120
 QY 1156 ctgtatgtgcagagaaatgtatcctttaaagaaggtgtggagcttcccaactgagat 1215
 Db 121 CTGTATGTGCGAGACAAATGATCCTTAAAGAGGTGTGGGTCTTTCCAACTGAGAT 180
 QY 1216 ttctgaagagctcagaagcttaataattatgcttgaagagatgtgagttcccaacc 1275
 Db 181 TTCTGAAGGTTTCAAGGTTCAATATTTAATGCTTCAAGGATGTGAGTTCCCAAC 240
 QY 1276 ttttgaagcaaaacctttagagaacacttaaaatataatgatacatgacacacacag 1335
 Db 241 TGTGAGCAAAAACCTTAGAGAAAACCTTAAATAATATGTAATGCGCAATACACAC 300
 QY 1336 taaggaacacatctctgttgaaggaacacacacacacacacacacacacacacac 1395
 Db 301 TACGACACACATTTCTGTGACAAAGGAAACCTTCAAAACATGTTCTTCCCTACCA 360
 QY 1396 caatagaacatgcagtaactaaagaacataatgtgtatllcccatglaattcctaag 1455
 Db 361 CAAGAAGAACATGACGTACTAAGCAATATATTGTGATTCCTCATATTTCTCAATG 420
 QY 1456 taacagtgcaagctctcttcgaagaagtaagatgacacagcgtcccttccctgtaca 1515
 Db 421 TAAACAGTGAAGTCTCTTTCGAAAGCTAAGATGACCATGCGCCCTTCTGTACATA 480
 QY 1516 taacttaagaagccccccccaacacacacacacacacacacacacacacacacacac 1575
 Db 481 TACCTTAAGAGAGCCGCCCTCCACACACACTGCCCCCAAGTATAGCGCATTTGACTG 540
 QY 1576 tgttatgtctatgtatgatagtcagaacacatgacatgacatgca-gtttcatattct 1634
 Db 541 TGTATATGTCTATGTATATGTCAAGAAACCATTAAGATTCATGACAGGGGTGATATCT 600
 QY 1635 tctagaatggaagtaataataatattgaaatgtgaaacacacacacacacacacacac 1685
 Db 601 TCTTAGATGGAAGTACTAATAATATTTTGAATGTGACACAGAGAGAA 651

RESULT 14

LOCUS BG619277 707 bp mRNA EST 18-APR-2001
 DEFINITION 602619402F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4733112 5',
 mRNA sequence.
 ACCESSION BG619277.1 GI:13670648
 VERSION BG619277.1
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

QY 1276 tgcagcaaaacccctaagagaacttaaaaaalatalgaatcacatgcgaatcacacagc 1335
DB 241 TGTACAGCAAAACCTTAGAGGAAACCTTAAAAATATATGATATACATGCCCAATACACAGC 300
QY 1336 taagacacacattcgttgacaaggaagaaaccttaaaagcatgttcttccctcaacca 1395
DB 301 TACAGACACACATTTCTGTGACACAGGAAACCTTCAAAGCATGTTCTTCCCTCACCA 360
QY 1396 caacagaacatgcagtaactaaagcaalatalattgattcccatgtaattcttcaatgt 1455
DB 361 CAACAGAACATGCAGTACTAAAGCAATATATTGTGATTCCTCCATGTAAATTTTCAATGT 420
QY 1456 taacagtgcaagtcctcttctgaaagctaagatgaacatgcgaccttccctctgacata 1515
DB 421 TAAACAGTGCAGTCTCTTCGAAAGCTAAGATGACCATGCGCCTTCTCTGTACATA 480
QY 1516 tacccttaagaagccccctccacacactgcccccaagatataatgcgcaattgactgtg 1575
DB 481 TACCTTAAGAAAGCCCTCCACACACTGCCCCCAGATATATGCGCATTTGTACTGCTG 540
QY 1576 tgttatatgctatgacatgltcagaacacatagcatgcatgcatgcatgcatgcatg 1635
DB 541 TGTATATGCTATGTATGATGTCAGAAACCATTAGCATGTCATGTCATGTCATGTCATG 600
QY 1636 ctaagatggaagtaataatataatt 1662
DB 601 CTAGATGTAGTAATATATTTGTT 627

Search completed: January 30, 2002, 03:23:44
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